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1 MRGATRVSIMLLLVTVSDCA......CSRFPDGRYRCSMDLKNINF 105
                                                                                      September 20, 2005, 12:35:04 ; Search time 165 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping. AAY66745 standard; protein; 105 AA. Membrane-bound protein PRO1186. 05-APR-2000 AAY66745; AAY6674

ALIGNMENTS

sapiens. WO9963088-A2

09-DEC-1999

99WO-US012252 02-JUN-1998; 02-JUN-1998; 02-JUN-1998; 03-JUN-1998; 02-JUN-1999;

98US - 0087607P.
98US - 0087609P.
98US - 0087827P.
98US - 0088021P.
98US - 0088028P.
98US - 008812P.
98US - 008811P.
98US - 0088734P.
98US - 0088741P.
98US - 0088741P.
98US - 0088710P. 04 - 70N - 1998 05 - 70N - 1998 10 - 70N - 1998 10 - 70N - 1998 10-JUN-1998; 10-JUN-1998; 10-JUN-1998; 0-JUN-1998

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98US-0088826P.
98US-0088861P.
98US-0088861P.
98US-0088863P.
98US-0089105P.
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98US-0089112P.
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The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were dentified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors. The Roce ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
Yuan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Membrane-bound proteins and related nucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Fig 266; 822pp; English.
           98US-0096012P

98US-0096143P

98US-0096329P

98US-0096757P

98US-0096768P

98US-0096773P

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17-AUG-1998;
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Sequence 105 AA;

Gaps ; 0 Length 105; 0; Indels Query Match 100.0%; Score 589; DB 3; Best Local Similarity 100.0%; Pred. No. 3.3e-54; Matches 105; Conservative 0; Mismatches 0;

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Š a disorders associated with the ovaries, cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders

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TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atlectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; schemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; alzheimer's Disease, cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262,
for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human and murine secreted proteins designated TANGO 216, 261, 266 and 267 useful as modulating agents of cellular processes, e.g. treating cancer.
HPGSHKVPPFRKRKHHTCPCLPNLLCSRPDGRYRCSMDLKNINF 105
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/note= "signal sequence"
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                                                                               AAB18453 standard; protein; 105 AA
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                                                                                                                                                 A human TANGO 266 polypeptide.
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N-PSDB; AAA75155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypotensive; orexigenic; antiallergic; antianginal; antimicrobial; antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia; allergy; angina pectoris; infection; MRSA; multiple resistant Staphylococcus aureus.
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Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a human TANGO 266 polypeptide. The specification also describes TANGO 262, TANGO 216, TANGO 261, and TANGO 267. TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor—associated disorder, regulate extracellular matrix structuring, cellular associated disorder, regulate extracellular matrix structuring, cellular andesion, and cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation, differentiation, and/or function of cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, cullmonary congestion or cedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, sphen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat
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Length 105

AAB68427 RESULT

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Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 105; Conservative 0;
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22-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zven1; 3p21.1; 3p14.3; Zven2; small cell lung cancer; wound healing; antitumour; antiinflammatory; necrosis; tissue growth; digestive enzyme; callular differentiation; gastrointestinal cell contractility; gastrointestinal motility; inflammation; hypermotility; diarrhoea; Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated Zven polypeptide useful for inhibiting proliferation of tumor cells, for treating small cell cancer of lung, to promote wound healing, and for treating Crohn's disease and diarrhea.
                                                                                                                                                                 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC
                                                                 Gaps
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   Length 105;
                                                                                                                                                                                                                                                              HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
                                                                                                                                                                                                                                                                                           61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
100.0%; Score 589; DB 4; Length 10 100.0%; Pred. No. 3.3e-54; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of a human Zven2 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB68427 standard; protein; 105
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25-FEB -2000; 2000US-00511879.
19-APR-2000; 2000US-00552203.
07-JUN-2000; 2000US-0210332P.
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                                                                 Matches 105; Conservative
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N-PSDB; AAF85427.
   Query Match
Best Local Similarity
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diarrhoea and Crohn's disease

Sequence 105 AA

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                                                        1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLMLRGLRMCTPLGREGEEC 60
                                            1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC
                      Gaps
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                                                                                       61 HPGSHKVPFPRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
                                                                                                  61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
                      0; Indels
; Score 589; DB 4;
; Pred. No. 3.3e-54;
0; Mismatches 0;
                                                                                                                                                                                                                                  Human PRO1186 polypeptide sequence.
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99WO-US028551
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99US-0170262P
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2000US-0187202P.
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2000WO-US022031
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AAU12172-AAU1246 represent novel human secretory and transmembrane PRO
polypeptides. The PRO polypeptides are useful to detect other PRO
polypeptides, to link biactive molecules to cells expressing PRO
polypeptides, to modulate biological activities of cells expressing PRO
polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumours by comparing PRO
polypeptide expression in a cell sample to that in a control sample. Some
of the 275 sequences are also useful to stimulate the release of tumour
cof the 275 sequences are also useful to stimulate the proliferation or
differentiation of chondrocytes, the proliferation or gene expression in
pericyte cells, the release of proteoglycans from cartilage, the
proliferation of inner ear utricular supporting cells or of T-
proliferation of inner ear utricular supporting cells or of T-
complepetides may modulate glucose or free faity acid uptake by skeletal
muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
VITA. The PRO polypeptides can be used in assays to identify molecules
involved in binding interactions. The polymucleotides encoding PRO
polypeptides can be used to generate probes, antisense RNA/DNA,
transgenic or knock out animals and can be used in gene therapy
                                                                                                                                                                                                                                                                                                                     Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
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                                                                                                                                                 Gao
                                                                                                                                            Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gr
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig 470; 813pp; English.
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US030952.
10-NOV-2000; 2000WO-US030873.
                                                                                                                                                                                                                                                                                                                                                                                                breast, prostate, cervical.
                                                                                              (GETH ) GENENTECH INC.
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1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC 100.0%; Score 589; DB 4; Length 105; 100.0%; Pred. No. 3.3e-54; Live 0; Mismatches 0; Indels Best Local Similarity 100. Matches 105; Conservative Query Match

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Gaps

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MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC

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61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105 .δ

RESULT 6 AAB53096

AAB53096 standard; protein; 105 AA

(first entry) 28-FEB-2001

Human angiogenesis-associated protein PRO1186, SEQ ID NO:165

Human; anglogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; anglogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Alzheimer's disease; Huntington's disease; stroke; drug screening; gene therapy; transgenic animal.

99WO-US012252. 99US-0141037P. 99US-0144758P. 99US-0145698P. 99WO-US020111. 99US-0123957P 05-JAN-2000; 200,0WO-US000219 99WO-US020594 99WO-US021090 99WO-US021547 99WO-US023089 99WO-US028313 99WO-US028409 99WO-US028565 WO200053753-A2. Homo sapiens. 30-NOV-1999; 02-DEC-1999; 01-SEP-1999 08-SEP-1999 14-SEP-2000 14-MAY-1999 02-JUN-1999 23-JUN-1999 20-JUL-1999 15-SEP-1999 15-SEP-1999 05-OCT-1999 30-NOV-1999

(GETH) GENENTECH INC.

Gerber H, Goddard A; Kuo SS, Mark MR, Marsters SA; illiams PM, Wood WI; Baker KP, Ferrara N, Gerber H, (Gurney AL, Hillan KJ, Kuo SS, Ma: ti RM, Watanabe CK, Williams PM, Ashkenazi AJ, Baker I Godowski PJ, Gurney Paoni NF, Pitti RM,

WPI; 2001-090793/10. N-PSDB; AAC97496. New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer.

Claim 69; Fig 66; 293pp; English.

The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AABS1064-BS1097), and to nucleic acids encoding RRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, agonists or antagonists of a PRO protein, and comprising a PRO protein, agonists or antagonists of a PRO protein, and comprising a PRO protein, agonists or antagonists of a PRO protein, and compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO comprosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid; and methods of inhibiting or stimulating endothelial compounds and methods of inhibiting or stimulating endothelial compounds and methods of inhibiting or stimulating endothelial compounds and protein, an agonist or antagonist thereof. PRO nucleic acids, PRO protein, or an agonist or antagonist thereof. Cardiovascular, endothelial or angiogenic disorders, such as agonists and PRO antoposins, may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as anderholist, rheumatcid arthritis, Crohn's disease, Huntington's diabetic retinopathy, rheumatcid arthritis, Crohn's disease, Huntington's candometriosis, ulcers, wounds, candometriosis ulcers, wounds, candometriosis proteins, as hybridiation probes to screen components or accomponents or proteins, and proteins, as hybridiation probes to screen the production of PRO proteins, as hybridiation probes to screen the production of PRO proteins, as hybridiation probes to screen the production of PRO proteins, as hybridiation probes to screen the production of PRO proteins, as hybridiation probes to screen t recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential therapeutic agents. the present sequence represents a PRO protein of the invention

Sequence 105 AA;

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proteins. The PRO proteins have cytostatic activity. The PRO proteins can radiolabels or antibodies, that cause cell death. PRO uncleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the issolation of human PRO sequences. AAF44070 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC 60
molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC
                                                              The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have curretains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO1186; PRO184; neoplastic; cell growth; tumour; cancer; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ovarian, renal, colorectal, uterine, prostate, lung, melanoma, central nervous system; leukemia, antitumor, cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                   Length 105;
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100.0%; Pred. No. 3.3e-54;
ive 0; Mismatches 0;
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ce= "N-myristoylation site"
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/note= "mature protein"
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                                              Claim 12; Fig 266; 935pp; English.
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99US-0145698P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO1186 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 105; Conservative
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/note=
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26-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRO polynucleotides used to produce polypeptides used to target bioactive
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                                                                                                  Godowski PJ;
Paoni NF;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
cancer; chromosomal mapping; gene mapping; tissue typing;
                                                                               MRGATRVSIMLLLVTVSDCAVITGACERDVOCGAGTCCAISLWLRGLRMCTPLGREGEEC
                                                  Gaps
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               Length 105;
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                                                                                                                                                 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
                                                                                                                                                                  HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
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                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                  Human PRO1186 (UNQ600) protein sequence SEQ ID NO:371.
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               Score 589; DB 4;
Pred. No. 3.3e-54;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                 AAB65268 standard; protein; 105 AA
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2000WO-US000376.
2000WO-US003565.
2000WO-US004341.
               100.0%;
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99WO-US030095.
99WO-US030911.
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99US-0149396P.
99WO-US021090.
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99US-0158663P.
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2000WO-US005841
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                                                                                                                                                                                                                                                                                                                                   (first entry)
             Query Match 100.
Best Local Similarity 100.
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostic assay.
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01-DEC-1999;
16-DEC-1999;
20-DEC-1999;
05-JAN-2000;
06-JAN-2000;
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22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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17-AUG-1999;
15-SEP-1999;
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08-OCT-1999
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Zhang Z;

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0; Gaps

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New human extracellular signaling nucleic acids and polypeptides useful for diagnosing, treating and preventing infections and gastrointestinal, neurological, reproductive, and autoimmune/inflammatory disorders.
                                                                                                    Claim 1; Page 89; 114pp; English.
                 2001-025021/03.
                           N-PSDB; AAC84303
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                                                                                                                                                                        The invention provides PRO1186 and PRO184 polypetides that can be used for the inhibition of neoplastic cell growth and for treating tumours. The PRO polypeptides can be expressed by standard recombinant methodology. The PRO polypeptides or their agonists are useful for inhibition of neoplastic cell growth and for treating tumours, cancers such as breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder or central nervous system cancers or melanoma and leukemia. The present sequence represents the human PRO1186 polypeptide (encoding cDNA)
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                                                                                                             Compositions for inhibiting neoplastic cell growth and treating tumor, cancer, comprises novel PRO1186 or PRO184 polypeptides or its agonist.
                                                                                                                                                                                                                                                                                                                                                                                MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC
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virucide; antibacterial; anti-HIV; human immunodeficiency virus;
antiinfertility; cerebroprotective; noortopic; antiulcer; antifungal;
anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extracellular signaling molecule; EXCS; anti-inflammatory; human;
                                                                                                                                                                                                                                                                                                                                                          ;
0
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                                                    Wood WI;
                                                                                                                                                                                                                                                                                                                                 Length 105;
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                                                    Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bandman O,
                                                                                                                                                                                                                                                                                                                              100.0%; Score 589; DB 4;
100.0%; Pred. No. 3.3e-54;
ive 0; Mismatches 0;
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                                                   Napier MA,
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                                                                                                                                                   Claim 31; Fig 2; 104pp; English
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99US-0144270P.
99US-0146700P.
 05-JAN-2000; 2000WO-US000219.
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                                                  Ashkenazi AJ, Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                        105; Conservative
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                         (GETH ) GENENTECH INC
                                                                           WPI; 2001-071078/08.
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                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                        N-PSDB; AAC84469
                                                                                                                                                                                                                                                                                                        Sequence 105 AA;
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                                                                                                                                                                                                                                                                               clone ID:
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The invention provides human extracellular signaling molecules (EXCS) and polynucleotides which identify and encode EXCS. EXCS can be expressed by standard recombinant methodology. The amino acid and nucleic acid sequences of EXCS are useful for diagnosing, treating and preventing infections and gastrointestinal (peptic ulcer, dysphagia, pancreatitis), certactions and gastrointestinal (peptic ulcer, dysphagia, pancreatitis), reproductive (infertility, ovulatory defects, endometriosis), autoimmune (infertility, actions, sequired immunodeficiency syndrome creproductive (infertility, ovulatory defects, endometriosis), autoimmune (infertility seases), and cell proliferative disorders including cancers (of the breast, adrenal gland, bone). They may also be used to creat fatal familial insomnia, nutritional and metabolic diseases of the nervous system, myopathies, mental disorders (anxiety, schizophrenia, nod), as well as infections caused by parasites (malaria, leishmania, crypanosoma), viral (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus, staphylococcus, bacillus), and fungal (aspergillus, crypanosoma), viral (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus, staphylococcus, bacillus), and fungal (aspergillus, antagonists, agonists, pharmaceutical compositions, and antibodies may also be used for treating or preventing disorders associated with the increased or decreased expression of EXCS may be correlated with the disease, to determine presence or excess expression of EXCS, to comply conclusions of associated disorders, as targets in microarray, to detect the presence of associated disorders, as targets in microarray, to detect the presence of associated disorders, as targets in microarray, also be used in diagnosing disorders, in monitoring patients being treated with EXCS agonists, in monitoring patients being created with EXCS of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRGATRVSIMLLLVTVSDCAVITGACBRDVQCGAGTCCAISLWLRGLRMCTPLGREGEBC
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Matches 105; Conserv
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The present sequence is that of a novel, tissue-restricted, growth and differentiation factor termed endocrine gland-derived vascular condifferentialian growth factor (EG-VEGF). The sequence is predicted from the open reading frame of a cDNA clone (see AAS91567) obtained from and copen reading frame of a cDNA clone (see AAS91567) obtained from the open reading frame of a cDNA clone (see AAS91567) obtained from an open reading frame of a cDNA clone (see AAS91567) obtained from an open copen in capillary endothelial cells derived from endocrine cglands, but has no effect on a variety of cother endochelial and noncodients and plote 9.05. The mature protein (mol.wt. 8600) is creatined with large connecting loops held together by disulfide bonds creatine and is predicted to consist of a series of short beta creatine with large connecting loops held together by disulfide bonds interactive surfaces. 80% Homology and 63% identity is shown to venom protein A (VPRA) of the black mamba snake, and 76% homology and 58% conditions associated with hormone-producing tissue, especially ovarian condition may be polycystic ovary syndrome, cancer, especially ovarian cancer, testicular cancer, prostate cancer or uterine cancer, or ovarian cancer, testicular cancer, prostate cancer or uterine cancer, or ovarian cancer, testicular cancer, prostate cancer or uterine cancer, or ovarian cancer, testicular and substitution or ovulation. Methods are claimed for identifying compounde that modulate EG-VEGF activity, and planting and planting of a planting or ovulation. Methods are calling a planting or prostate envised in the planting or survived in the planting or survived and planting or survived and planting or survived and planting or survived and survived survi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New endocrine gland-vascular endothelial growth factor (EG-VEGF) polypeptides, agonists and antagonists, useful for regulating fertility, and for treating cancer of the reproductive organs, e.g. ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  especially the ability to induce phosphorylation of a kinase involved acell proliferation or survival, to induce chemotaxis, angiogenesis, or cell differentiation, or to induce endothelial cell proliferation
                                                                                                                                                                                                                                                                                                         'note= "N-myristoylated"
                                                                                                                                                                                                                                                                                                                                                                                                       note= "N-myristoylated"
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                                                    1. .19
/label= Signal_peptide
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Location/Qualifiers
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07-SEP-2000; 2000US-0230978P.
01-DEC-2000; 2000WO-US032678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-130882/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JAN-2002
                                              Peptide
                                                                                                                                                       Protein
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One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or liver tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polymodisotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goddard A, Godowski PJ;
phan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                         secreted protein; PRO; tumour; lung cancer; colon cancer;
                                                                                                                                                                                                   breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; tumour necrosis factor-alpha.
             61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen ME, Goddard
Smith V, Stephan JF,
                                                                                      AAU83674 standard; protein; 105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Fig 166; 359pp; English.
                                                                                                                                                                 Human PRO protein, Seg ID No 166.
                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0220638P
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0220666P.
2000US-0220893P.
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2001WO-US006666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001US-00816744.
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                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
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N-PSDB; ABK33618.
                                                                                                                                                                                                                                                                                  WO200208288-A2.
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10-NOV-2000;
28-NOV-2000;
01-DEC-2000;
20-DEC-2000;
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25-JUL-2000;
25-JUL-2000;
25-JUL-2000;
25-JUL-2000;
26-JUL-2000;
                                                                                                                                                                                                                                                           Homo sapiens.
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22-AUG-2000;
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25-JUL-2000;
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                                                              RESULT 11
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1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC

100.0%; Score 589; DB 5; Length 105; 100.0%; Pred. No. 3.3e-54;

0; Mismatches

Local Similarity 100.

Matches

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Query Match

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cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human blood, fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapphing. AAU83592-AAU83713 represent human PRO protein sequences of the invention
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 The PRO polypeptides are useful for diagnosing tumours, especially lung
                                                                                                                                                                                                                                                                                                                              1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC
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                                                                                                                                                                                                                                                             Length 105;
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                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                            100.0%; Score 589; DB 5; 100.0%; Pred. No. 3.3e-54;
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                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB84902 standard; protein; 105 AA
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2000US-0220624P.
2000US-0220664P.
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2000US-00664610.
2000US-00665350.
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17-AUG-2000; 2000US-00643657.
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2000WO-US030873
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2000US-00747259
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 105; Conservative
                                                                                                                                                                                                                           Sequence 105 AA;
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18-SEP-2000; 2
18-SEP-2000; 2
24-OCT-2000; 2
08-NOV-2000; 2
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28-JUL-2000;
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20-DEC-2000;
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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynuclectides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynuclectides, proteins, agonists and antagonists are useful for treating or diagnosing cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycardial infarctions, thrombophlebitis, lymphanogitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC
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                                                                                                                                                                                                                                                                                                                                                  Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                 Goddard A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human physiologically-active ZAQ ligand-related protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAO15527 standard; protein; 105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Fig 172; 565pp; English.
              2001US-00767609.
2001US-00796498.
2001WO-US006520.
                                                                                                                 2001US-00816744.
2001US-00828366.
2001US-00854208.
                                                                                                                                                                                       2001US-00866028.
2001US-00866034.
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2001WO-US017443.
                                                                                2001US-00802706
2001US-00808689
                                                                 2001WO-US006666
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                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 105 AA;
              22-JAN-2001;
28-FEB-2001;
28-FEB-2001;
01-MAR-2001;
                                                                                09-MAR-2001;
14-MAR-2001;
                                                                                                                   22-MAR-2001;
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10-MAY-2001;
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(TAKE ) TAKEDA CHEM IND LTD
                           Masuda Y,
                                                           WPI; 2002-188546/24
N-PSDB; ABL49637.
                                                                                                                                                                                                                                                                          present invention
                                                                                                                                                                                                                                                                                              Sequence 105 AA;
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                                                                                                               like colitis,
gene therapy
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                           Ohtaki T,
Hinuma S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises a method for producing an active peptide that has the same activity as a ZAQ ligand isolated from eukaryotic cells. The method of the invention is useful for the production of a physiologically -active ZAQ ligand for use in preventing or treating digestive diseases (e.g. colitis and diarrhea). The present amino acid sequence represents a human physiologically active ZAQ ligand-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G protein-coupled receptor; ZAQ ligand; physiologically active peptide; ZAQ; antidiarrheic; laxative; drug development; digestive disease; colitis; diarrhoea; constipation; poor-absorption syndrome; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                   Industrial production of physiologically-active ZAQ ligand by expressing in transformant prokaryote and refolding in redox buffer, for use in preventing or treating digestive diseases e.g. colitis and diarrhea.
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC 60
Human, ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;
colitis; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:23.
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0
                                                                                                                                                                                                                                                                                                                                                                               Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
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100.0%; Pred. No. 3.3e-54;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                            Example 3; Page 76-77; 93pp; Japanese
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                                                                                                   21-JAN-2002; 2002WO-JP000378
                                                                                                                       22-JAN-2001; 2001JP-00013027
17-MAY-2001; 2001JP-00147759
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02-FEB-2001; 2001JP-00026779
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Les 105; Conservative
                                                                                                                                                                           Suenaga M,
                                                                                                                                                                                                WPI; 2002-566801/60
                                                                                                                                                                                                                                                                                                                                                          Sequence 105 AA;
                                                         WO200257443-A1
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                                      Homo sapiens
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                                                                              25-JUL-2002
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                                                                                                                                                                           Yamada T,
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The present invention describes a peptide containing an amino acid sequence (I) identical to or substantially similar to that of the sequences in ABB06305 or ABB06306, or its salt. (I) has antidiarrheic and laxative activities. The peptide decoding DNAs from the present invention are useful for developing drugs to treat digestive diseases like colitis, diarrhoea, constipation and poor-absorption syndrome, including gene therapy. The physiologically-active cows milk-originated peptides are applicable as a specific ligand of brain-originated orphan G protein-coupled receptor protein ZAO. ABL49615 to ABB40659 and ABB06303 to ABB06315 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                    Physiologically-active peptides from cows milk, useful for developing drugs to treat ZAQ-mediated diseases, particularly digestive diseases like colitis, diarrhea, constipation and poor-absorption syndrome, by
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Υ;
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   Terao Y,
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/note= "Mature human prokineticin 1"
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; Pred. No. 3.3e-54;
0; Mismatches 0;
   Watanabe T,
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/label= Signal_peptide
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Takatsu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE24382 standard; protein; 105
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Best Local Similarity 100.
Matches 105; Conservative
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The invention relates to human prokineticin 1 and 2 polypeptides that stimulate gastrointestinal smooth muscle contraction and nucleic acid molecules encoding such polypeptides. Polypeptides of the invention are useful for treating disorders involving impaired gastrointestinal motility. They are useful for stimulating gastrointestinal motility in abisorders such as irritable bowel syndrome, diabetic gastroparesis, postoperational ileus, chronic constipation and gastrointestinal reflux disease. The prokineticin antagonists are useful for inhibiting gastrointestinal motility in conditions of diarrhoea, malabsorptive disorders, inflammatory bowel disorders, infectious diseases and intestinal cancers. The antagonists also act as analgesics. The present sequence is human prokineticin 1 precursor protein
                                                                                                                                          New isolated human prokineticin 1 and 2 polypeptides that stimulate gastrointestinal smooth muscle contraction, useful for improving impaired gastrointestinal motility in irritable bowel syndrome, chronic constipation.
                                                                                                                                                                                                                                                                    Example 1; Fig 1; 86pp; English.
(REGC ) UNIV CALIFORNIA.
                                                                                       WPI; 2002-479752/51.
N-PSDB; AAD39321.
                                              Ehlert FJ;
                                              Zhou Q,
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Sequence 105 AA;

0; Gaps 100.0%; Score 589; DB 5; Length 105; 100.0%; Pred. No. 3.3e-54; Live 0; Mismatches 0; Indels Best Local Similarity 100. Matches 105, Conservative Query Match

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Search completed: September 20, 2005, 12:55:58 Job time : 167 secs

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SEQ ID NO 5
LENGTH: 105
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Sequence 7146, Ap
Sequence 13, Appl
Sequence 12, Appl
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11, Appl
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Sequence 4698, Ap
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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-12-202-2

US-10-212-202-2

US-10-212-355-2

US-09-161-241-14

US-09-161-241-13

US-09-161-241-31

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US-09-905-125A-236

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Listing first 45 summaries
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Sequence 10, Appl
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Sequence 5, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 13, Appli
Sequence 2, Appli
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     US-09-161-241-10
US-09-976-7-1086
US-09-961-7099-13
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US-09-949-016-11293
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100.0%; Pred. No. 9.3e-59;
tive 0; Mismatches 0;
Sequence 5, Application US/09712529
Patent No. 6485938
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Thompson, Penny P.
TITLE OF INVENTION: Human Zven Proteins
FILE REFERENCE: 99-81
CURRENT APPLICATION NUMBER: US/09/712,529
CURRENT PILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                             FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapiens
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APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
APPLICANT: Bishop, Paul D.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Thompson, Penny P.
TITLE OF INVENTION: Human Zven Proteins
FILE REFERENCE: 99-81
CURRENT APPLICATION NUMBER: US/10/212,201A
CURRENT FILING DATE: 2002-08-02
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 7 Sequence 5, Application US/10212201A Patent No. 6756479 GENERAL INFORMATION:

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NAME/KEY: SIGNAL
LOCATION: -19...1
NAME/KEY: UNSURE
LOCATION: 38
OTHER INFORMATION: Xaa = Ala,Gly
                                                                                                            US-09-621-976-5350
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Facent No. 6639063
GENERAL INFORMATION:
APPLICANT: Johert, S.
APPLICANT: Johert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENERIO C94PR2.
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5350
LENGTH: 105
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Sequence 5, Application US/10212355
Sequence 5, Application US/10212355
Sequence 5, Application US/10212355
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul D.
APPLICANT: Thompson, Paul D.
APPLICANT: Thompson, Paul D.
APPLICANT: Thompson, Penny P.
TITLE OF INVENTION: Human Zven Proteins
FILE REFERENCE: 99-81
CURRENT APPLICATION NUMBER: US/10/212,355
CURRENT FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASESEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
FEATURE:
                                                                                    ORGANISM: Homo sapiens
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APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.02.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
FRIOR APPLICATION NUMBER: US 60/122,487
FRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SEQ ID NO 4698
LENGTH: 80
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                                                                                                                                              1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGRKXEEC 60
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                                                           0; Gaps
Query Match 98.0%; Score 577; DB 4; Length 105; Best Local Similarity 97.1%; Pred. No. 2.1e-57; Matches 102; Conservative 2; Mismatches 1; Indels
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Patent No. 6485938;
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.;
APPLICANT: Bishop, Paul D.;
APPLICANT: Whitmore, Theodore E.;
APPLICANT: Thompson, Penny P.;
TITLE OF INVENTION: Human Zven Proteins;
FILE REFERENCE: 99-81;
CURRENT APPLICATION NUMBER: US/09/712,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: -19..-1

JOTHER INFORMATION: SCORE 7.2

CHER INFORMATION: SEQ VSIMLLLVTVSDC/AV

US-09-513-999C-4698
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4698, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
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Matches 79; Conservative
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
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201 LC 202
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US-09-161-241-14
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US-09-161-241-14
                                                                                                                                              US-10-212-355-2
              SEQ ID NO 2
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Sequence 2, Application US/10212201A

Patent No. 6756AD

GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

APPLICANT: Whitmore, Theodore E.

APPLICANT: Whitmore, Theodore E.

FILE REFERENCE 99-81

FILE REFERENCE 99-81

CURRENT APPLICATION NUMBER: US/10/212,201A

CURRENT FILING DATE: 2002-08-02

PRIOR PILING DATE: 2000-11-14

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2.

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| Patent No. 6828425 | GENERAL INPORMATION: APPLICANT: Sheppard, Paul O. APPLICANT: Bishop, Paul D. APPLICANT: Thompson, Penny P. TILE REFERENCE: 99-81 CURRENT APPLICATION: Human Zven Proteins | TILE REFERENCE: 99-81 CURRENT FILING DATE: 2002-08-02 | NUMBER OF SEQ ID NOS: 7 | SOFTWARE: FastSEQ for Windows Version 3.0
CURRENT FILLING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PastSEQ for Windows Version 3.0
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                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-09-712-529-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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US-10-212-201A-2
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                                                                                                   SEQ ID NO 2
LENGTH: 108
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US-10-212-355-2
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Sequence 7146, Application US/09949016

Patent No. 6812339

Patent No. 6812339

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PELING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-00-08

NUMBER: OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7146
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                                                                                                                                                                                                               Gaps
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                                                                                                                                                  Length 108;
                                                                                                                                                                                                         24; Indels
                                                                                                                                               Query Match 51.4%; Score 303; DB 4; Best Local Similarity 55.2%; Pred. No. 1.2e-26; Matches 48; Conservative 15; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09161241
Petent No. 6344541
GENERAL INFORMATION:
APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars B
APPLICANT: Theill, Lars B
APPLICANT: Theill, Lars B
APPLICANT: Mang, Daguang
ITILE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
ILENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                        78 FGRRMHHTCPCLPGLACLRTSFNRFIC 104
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LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-161-241-11
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                                                                                                                                                        Gaps
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                                                                                                       Score 102; DB 4; Length 186;
Pred. No. 0.00084;
8; Mismatches 30; Indels
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; Sequence 12, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Flatili, Lars B
; APPLICANT: Theill, Lars B
; APPLICANT: Theill, Lars B
; APPLICANT: Theill, Lars B
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12.
ILENGTH: 259
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13. Application US/09161241
; Betent No. 6344541
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Wang, Daquang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
TILE REPERENCE: A-548
CURRENT APPLICATION UNDBER: US/09/161,241
CURRENT PILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver: 2.0
; SEQ ID NO 13.
                                                                                                       Query Match
Best Local Similarity 31.5%;
Matches 23; Conservative
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Best Local Similarity
Matches 23; Conserval
LENGTH: 186
TYPE: PRT
ORGANISM: Human
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ORGANISM: Human
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US-09-161-241-12
                                                              US-09-949-016-7146
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US-09-161-241-12
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US-09-161-241-13
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US-09-949-016-6872

Sequence 6872, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSESEEQ for Windows Version 4.0

SEC ID NO 6872

LENGTH: 259
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                                                           30; Indels 12; Gaps
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Query Match
17.3%; Score 102; DB 3; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0012;
Matches 23; Conservative 8; Mismatches 30; Indels
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Pred. No. 0.0012;
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; Patent No. 6344541
; Patent No. 6344541
; GENERAL INFORMATION:
   APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Theill, Lars E
; APPLICANT: WINST DATE
; TILE REFERENCE: A-548
; TILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 11
; LEMGTH: 259
; TYPE: PRT
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Best Local Similarity 31.5%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                 235 KGLSCKVWKDATY 247
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235 KGLSCKVWKDATY 247
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US-09-949-016-6872
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                                                                                                             183 CLRSSDCIDGFCCARHFW---TKICKPVLHQGEVCTKQRKKGSHGLEIFQR-----CDCA 234
                                                                          26 CERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC----HPGSHKVPFFRKRKHHTCPCL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
17.1%; Score 100.5; DB 3; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.0025;
Matches 26; Conservative 3; Mismatches 29; Indels 11; Gaps
Best Local Similarity 31.5%; Pred. No. 0.0016;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09161241
| Patent No. 634541
| GENERL INFORMATION:
| APPLICANT: Bass, Michael B
| APPLICANT: Sullivan, John K
| APPLICANT: Whill, Lars E
| APPLICANT: Holl, Lars E
| APPLICANT: 1998-09-25
| CURRENT FILING DATE: 1998-09-25
| NUMBER OF SEQ ID NOS: 78
| SOGTWARE: Patentin Ver. 2.0
| SEQ ID NO 9
| LENGTH: 350
| TYPE: PRT
| ORGANISM: Human
| US-09-161-241-9
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US-09-161-241-9
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Search completed: September 20, 2005, 13:00:32 Job time : 43 secs

78 CPCLPNLLC 86 ||| ||| ||| 265 CPCASGLLC 273

208 CDNQRDCQPGLCCAFQ---RGLLFPVCTPLPVEGELCHDPASRLLDLITWELEPDGALDR 264

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26 CERDVOCGAGTCCAISLWLRGL--RMCTPLGREGEECH-PGSHKVPFFRKRKH-----HT 77

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730910ES: US/09/989,722
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 371, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Napier, Mary A.
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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                                                                                                  September 20, 2005, 12:59:06; Search time 168 Seconds (without alignments) 253.080 Million cell updates/sec
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Sequence 371,
Sequence 371,
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Sequence 371,
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22: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-989-723-371
US-09-989-273-371
US-09-989-731-371
US-09-989-732-371
US-09-991-073-371
US-09-991-163-371
US-09-991-163-371
US-09-991-163-371
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US-09-991-163-371
US-09-991-073-371
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Maximum Match 100%
Listing first 45 summaries
                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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                                                                     OM protein
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100 100 100 100 100 100 100 100 100 100	105
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	000
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ALIGNMENTS

Paoni, Nicholas F.

PRIOR APPLICATION NUMBER: 60/64276
PRIOR PALING PATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/66226
PRIOR PILLING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/665311
PRIOR PELLING DATE: 1997-11-13
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PRIOR PELLING DATE: 1998-0-6-30
PRIOR PELLING DATE: 1998-0-6-

PRIOR FILING DATE: 1938-06-12

PRIOR PLING DATE: 1938-06-16

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PRIOR PLILING DATE: 1938-06-17

PRIOR PLILING DATE: 1938-06-18

PRIOR PLILING DATE: 1938-06-19

PRIOR PLILING DATE: 1938-06-24

PRIOR PLILING DATE: 1938-06-25

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R FILING DATE: 1997-11-13
R APPLICATION NUMBER: 60/066770
R FILING DATE: 1997-11-24
R PLING DATE: 1998-02-25
R PLING DATE: 1998-02-25
R APPLICATION NUMBER: 60/078910
                                                                                                                                                                                                                                                                                                                                    R APPLICATION NUMBER: 60/087106
R FILING DATE: 1998-05-28
R APPLICATION NUMBER: 60/087607
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R APPLICATION NUMBER: 60/08759
R APPLICATION NUMBER: 60/087878
R FILING DATE: 1998-06-02
R APPLICATION DATE: 1998-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088025

R RILING DATE: 1998-06-04

R RILING DATE: 1998-06-04

R FILING DATE: 1998-06-04

R FILING DATE: 1998-06-07

R FILING DATE: 1998-06-07

R FILING DATE: 1998-06-07
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R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/086033
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R APPLICATION NUMBER: 60/08655
R FILING DATE: 1998-06-09
R FILING DATE: 1998-06-10
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088738
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R APPLICATION NUMBER: 60/088167
R FILING DATE: 1998-06-05
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R APPLICATION NUMBER: 60/088658
R FILING DATE: 1998-06-11
R FILING DATE: 1998-06-11
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/08861
                                  APPLICATION NUMBER: 60/065186
FILING DATE: 1997-11-12
APPLICATION NUMBER: 60/065311
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089440
FILING DATE: 1998-06-16
                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/088217
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APPLICATION NUMBER: 60/08826
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 105;
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100.0%; Score 589; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1938-06-26
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PRIOR PLING DATE: 1938-07-01
PRIOR APPLICATION NUMBER: 60/09136
PRIOR PILING DATE: 1938-07-02
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PRIOR PELING DATE: 1998-07-07
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Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: ABINEMAZI, AVI J.
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Grimaldi, J. Christopher
Gurney, Austin L.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Botstein, David
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Eaton, Dan L.
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US-09-989-723-371
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PRICE APPLICATION NUMBER: 60/09512
PRICE APPLICATION NUMBER: 60/09514
PRICE PLILING DATE: 1998-06-16
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PRICE PLILING DATE: 1998-06-18
PRICE PLILING DATE: 1998-06-22
PRICE PLILING DATE: 1998-06-24
PRICE PLILING DATE: 1998-06-25
PRICE PLILING DATE: 199
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ö 9 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLMLRGLRMCTPLGREGEEC 60 APPLICANT: CHANGE CONTRIBUTION. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PLC56
CURRENT APPLICATION NUMBER: US/09/989,279
FRICH APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PAPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PILING DATE: 1997-11-12 1 MRGATRVSIMILLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC Gaps ; Length 105; 61 HPGSHKVPFFRKRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105 Indels Query Match 100.0%; Score 589; DB 9; Best Local Similarity 100.0%; Pred. No. 1.4e-53; Matches 105; Conservative 0; Mismatches 0; PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 6//091360
PRIOR PLING DATE: 1998-07-01
PRIOR APLING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07 Sequence 371, Application US/09989279
Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICANT: ABARCHAZI, AVI J. Grimaldi,J.Christopher Gurney, Austin L. Kljavin,Ivar J. Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I. Fong, Sherman Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey Ferrara, Napoleone Godowski, Paul J. Baker, Kevin P. Botstein, David Napier, Mary A. Desnoyers, Luc Eaton, Dan L. Pan,James RESULT 3 US-09-989-279-371 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT APPLICANT g ò

NUMBER: 60/065311 1997-11-13 NUMBER: 60/06670 1997-11-24 NUMBER: 60/075945 1998-02-25 NUMBER: 60/078910 1998-03-20 NUMBER: 60/08312 1998-04-28 NUMBER: 60/08460 1998-05-07 NUMBER: 60/08460 1998-05-07 NUMBER: 60/08460	1998 06-02 1998 - 06-02 1998 - 06-02 1998 - 06-02 1998 - 06-02 1998 - 06-02 1998 - 06-02 1998 - 06-02 1998 - 06-03 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-04 1998 - 06-05	NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06 NUMBER: 1998-06
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PRIOR FILING DATE: 1998-06-16

PRIOR PLILAGION UNDERS: 60/08538

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PRIOR PLILACATION UNDERS: 60/08559

PRIOR PLILACATION UNDERS: 60/08599

PRIOR FILING DATE: 1998-06-17

PRIOR PLILACATION UNDERS: 60/08509

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R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/087106
R FILING DATE: 1998-05-28
R APPLICATION NUMBER: 60/087607
R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087609
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R APPLICATION DATE: 1998-06-02
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R FILING DATE: 1998-06-10
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R APPLICATION NUMBER: 60/08824
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R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088976
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APPLICATION NUMBER: 60/075945
FILING DATE: 1998-02-25
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FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
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APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/088217
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FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/088167
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100.0%; Pred. No. 1.4e-53;
iive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1988-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09163
PRIOR PELING DATE: 1998-07-07
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PRIOR FILING DATE: 1997-06-16
PRIOR PELING DATE: 1997-06-16
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/065311
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Patent No. US20020072497A1
GENERAL INFORMATION:
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Gurney, Austin L.
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Ferrara, Napoleone
Fong, Sherman
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Roy, Margaret Ann
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Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 105; Conservative
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Best Local Similarity
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US-09-989-727-371
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REJOR PELLOCATION NUMBER: 60/089538
PRIOR PELLOCATION NUMBER: 60/089598
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PRIOR PELLOCATION NUMBER: 60/089901
PRIOR PELLOCATION NUMBER: 60/090401
PRIOR PELLOCATION NUMBER: 60/090601
PRIOR PELLOCATION NUMBER: 60/0

APPLICANT: Stewart, Time, Ann.
APPLICANT: Stewart, Time, Ann.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Walliams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Shang, Zemin
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PL70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1998-02-25 9 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC Gaps . 0 Query Match 100.0%; Score 589; DB 9; Length 105; Best Local Similarity 100.0%; Pred. No. 1.4e-53; Matches 105; Conservative 0; Mismatches 0; Indels 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105 PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07 Sequence 371, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Bakhenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David Grimaldi,J.Christopher Gurney,Austin L. Kljavin,Ivar J. Napier,Mary A. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Watanabe, Colin K. Williams, P. Mickey Wood, William I. Ferrara, Napoleone Fong, Sherman Gerber, Hanspeter Pan, James Paoni, Nicholas F. FILING DATE: 1998-07-01 Gerritsen, Mary E. Goddard, Audrey Desnoyers, Luc Eaton, Dan L. Godowski, Paul RESULT 5 US-09-989-731-371 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: ઠે

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NUMBER: 60 1998-03-6 NUMBER: 60 1998-04-2 NUMBER: 60 1998-05-0 NUMBER: 60 1998-06-0 1998-06-0 1998-06-0 NUMBER: 60	06-03 06-04 06-05 06-06 06-06 06-06 06-06 06-07 06-08 06-08 06-08 06-09 06	NUMBER: 60/088742 1998-06-10 1998-06-10 1998-06-10 1998-06-10 1998-06-10 NUMBER: 60/08826 1998-06-10 NUMBER: 60/08861 1998-06-11 1998-06-11 NUMBER: 60/08876 1998-06-11 NUMBER: 60/08976 1998-06-12 NUMBER: 60/089105 1998-06-12 NUMBER: 60/089105 1998-06-16 NUMBER: 60/089112 1998-06-16 NUMBER: 60/089512 1998-06-16 NUMBER: 60/089513 1998-06-16 NUMBER: 60/089514 1998-06-16 NUMBER: 60/089514 1998-06-16 NUMBER: 60/089513
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PRIOR PILING DATE: 1998-06-25
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R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/08326

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R APPLICATION NUMBER: 60/088217

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R FILING DATE: 1998-06-04
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R APPLICATION NUMBER: 60/088021
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APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088824
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APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089514
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       FILING DATE: 1998-04-28
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CURRENT APPLICATION NUMBER: US/09/989,732

CURRENT PILING DATE: 2001-11-19

PRIOR PILING DATE: 1997-06-16

PRIOR PILING DATE: 1997-06-16

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-11-12

PRIOR PILING DATE: 1997-11-12

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PRIOR PILING DATE: 1997-11-14
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100.0%; Pred. No. 1.4e-53;
Live 0; Mismatches 0;
                     R FILING DATE: 1998-07-02
R APPLICATION WUMBER: 60/091633
R FILING DATE: 1998-07-02
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R FILING DATE: 1998-07-07
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R FILING DATE: 1998-07-09
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Patent No. US20020123463A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/078910
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Gurney, Austin L.
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Pan, James
Paoni, Nicholas F.
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Srewart, Timothy A.
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Watanabe, Colin K.
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Gerritsen, Mary E.
Goddard, Audrey
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Best Local Similarity 100.
Matches 105; Conservative
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R APPLICATION NUMBER: 60/089600
R FILING DATE: 1998-66-17
R APPLICATION NUMBER: 60/089633
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089908
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R APPLICATION NUMBER: 60/089948
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R FILING DATE: 1998-06-29
R APPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-29
R APPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090355
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090439
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090439
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R APPLICATION NUMBER: 60/090435
R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090557
R APPLICATION NUMBER: 60/090676
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090678
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090690
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090691
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090695
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R APPLICATION NUMBER: 60/090695
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R APPLICATION NUMBER: 60/090605
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APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091626
FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/091478
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
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             REPRESENTED BY THE PROPERTY OF THE PROPERTY OF
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ö 9 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC 60 APPLICANT: Zhang, Zemin TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PICIS Gaps 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC ; Length 105 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105 61 HPGSHKVPPFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105 0; Indels 100.0%; Score 589; DB 9; 100.0%; Pred. No. 1.4e-53; iive 0; Mismatches 0; RESULT 7
US-09-991-073-371
sequence 371, Application US/09991073
Fatent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P. PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09 Grimaldi, J. Christopher Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I. Ferrara, Napoleone Gerritsen, Mary E. Gurney, Austin L. Gerber, Hanspeter Kljavin, Ivar J. Napier, Mary A. Query Match Best Local Similarity 100. Matches 105; Conservative Goddard, Audrey Godowski, Paul Desnoyers, Luc Fong, Sherman Eaton, Dan L. Pan, James APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: 8 ò g

NUMBER: 60/087106 1998-05-28 NUMBER: 60/087607 1998-06-02 1998-06-02 1998-06-02 1998-06-02 1998-06-02 NUMBER: 60/08759 1998-06-03 NUMBER: 60/08021 1998-06-04 NUMBER: 60/088025 1998-06-04 NUMBER: 60/088026 1998-06-04 NUMBER: 60/088026	1998- 1998-	06-16 06-16 06-16 06-17 06
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PRIOR APPLICATION NUMBER: 60/089532
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PRIOR PILING DATE: 1998-06-17
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100.0%; Score 589; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-17
PRIOR PELICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-05-07
PRIOR PELICATION NUMBER: 60/08310
PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/084600
PRIOR PLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
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Patent No. US2002013252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
          PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR PILING DATE: 1998-07-09
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Grimaldi, J. Christopher
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Paoni, Nicholas F.
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Napier, Mary A.
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Botstein, David
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R FILING DATE: 1998-06-19
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R APPLICATION NUMBER: 60/090678
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R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090694 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182 APPLICATION NUMBER: 60/089907 APPLICATION NUMBER: 60/091478 APPLICATION NUMBER: 60/091544 FILING DATE: 1998-07-01 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 PRILICA RELIGIOR PRILIC

APPLICANT: Stowart Timothy A. APPLICANT: Stowart Timothy A. APPLICANT: Stowart Timothy A. APPLICANT: Stowart Timothy A. APPLICANT: Tumas D. Daniell R. APPLICANT: Tumas D. Daniell R. APPLICANT: Watenabe, Colin K. APPLICANT: Williams P. Mickey APPLICANT: Wood, Williams P. Mickey APPLICANT: Whilliams P. Mickey APPLICANT: Williams P. Mickey APPLICANT: Wood, William I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Socreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION NUMBER: 60/09991,163
CURRENT PILING DATE: 1997-00-17
CURRENT PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06536
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PELING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PELING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/08360
PRIOR APPLICATION NUMBER: 60/087609
PRIOR APPLICATION NUMBER: 60/087609 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEBC 60 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC Gaps ö Length 105; 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105 Indels ; Score 589; DB 9; ; Pred. No. 1.4e-53; 0; Mismatches 0; Sequence 371, Application US/09991163 Patent No. US20020132253A1 GENERAL INFORMATION: Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L. Query Match 100.0%; Best Local Similarity 100.0%; Matches 105; Conservative 0; Ferrara, Napoleone Pan, James Paoni, Nicholas F. Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey Kljavin, Ivar J. APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. Botstein, David Napier, Mary A. Desnoyers, Luc Fong, Sherman Eaton, Dan L. RESULT 9 US-09-991-163-371 APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT ò 셤

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PRIOR PILLING DATE: 1939-06-03
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PRIOR PILLING DATE: 1939-06-03
PRIOR PELLING DATE: 1939-06-04
PRIOR APPLICATION NUMBERS: 60/08025
PRIOR PAPLICATION NUMBERS: 60/08025
PRIOR APPLICATION NUMBERS: 60/08025
PRIOR APPLICATION NUMBERS: 60/08026
PRIOR APPLICATION NUMBERS: 60/08029
PRIOR PILLING DATE: 1939-06-04
PRIOR PILLING DATE: 1939-06-05
PRIOR PILLING DATE: 1939-06-10
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PRIOR FILING DATE: 1998-06-19
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PRIOR APPLICATION UNMERS: 60/08948
PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-23
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-07-01
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Query Match

100.0%; Score 589; DB 9; Length 105;

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PRIOR FILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-05
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PRIOR PILING DATE: 1998-06-09
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08858
PRIOR PILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08858
PRIOR PILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08951
PRIOR PILING DATE: 1998-06-11
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PRIOR PILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08951
PRIOR PILING DATE: 1998-06-17
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R APPLICATION NUMBER: 60/088026

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088028

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R APPLICATION NUMBER: 60/088029

R APPLICATION NUMBER: 60/0880303

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R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088033

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088336
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PRIOR PILING DATE: 1998-06-18
PRIOR PLING DATE: 1988-06-18
PRIOR FILING NAME: 60/089908
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APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C25
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tive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/993,604
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PELLING DATE: 1997-06-16
PRIOR PELLING DATE: 1997-06-16
PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-24
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PRIOR PELLING DATE: 1997-11-24
PRIOR PELLING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/076945
PRIOR PELLING DATE: 1998-02-25
PRIOR PELLING DATE: 1998-02-26
PRIOR PELLING DATE: 1998-04-28
PRIOR PELLING DATE: 1998-05-07
PRIOR PELLING DATE: 1998-05-07
PRIOR PELLING DATE: 1998-05-07
PRIOR PELLING DATE: 1998-05-07
PRIOR PELLING DATE: 1998-06-02
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Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Paton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Forg, Sherman
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Best Local Similarity 100. Matches 105; Conservative
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APPLICANT: Key, Margaret Ann
APPLICANT: Tumes, Daniel
APPLICANT: Tumes, Daniel
APPLICANT: Tumes, Daniel
APPLICANT: William: P. Mickey
APPLICANT: William: P. Mickey
APPLICANT: William: P. Mickey
APPLICANT: Mod, William: P. Mickey
APPLICANT: Along, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted 
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                                           61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
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APPLICANT: Ashkenazi, Avi J.
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Grimaldi, J.Christopher
Gurney, Austin L.
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Paoni, Nicholas F.
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Goddard, Audrey
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Gerber, Hanspeter
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PRIOR APPLICATION NUMBER: 60/08958
PRIOR FILING DATE: 1998-06-19
PRIOR PLICATION NUMBER: 60/08052
PRIOR FILING DATE: 1998-06-19
PRIOR PLILING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-22
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PRIOR PLING DATE: 1998-06-23
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PLING DATE: 1998-06-25
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PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-26
PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09163
PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09193
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PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09193
PRIOR PLING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-03
PRIOR PLING DATE: 1998-07-03
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Query Match 100.0%; Score 589; DB 9; Length 105; Best Local Similarity 100.0%; Pred. No. 1.4e-53; Matches 105; Conservative 0; Mismatches 0; Indels

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PRIOR PLILING DATE: 1998-06-26
PRIOR PLILING DATE: 1998-06-27
PRIOR APPLICATION NUMBER: 60/09069
PRIOR PLILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/09150
PRIOR PLILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/09150
PRIOR PRIOR PLICATION NUMBER: 60/09150
PRIOR APPLICATION NUMBER: 60/091

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Length 105; Indels

100.0%; Score 589; DB 9; 100.0%; Pred. No. 1.4e-53; iive 0; Mismatches 0;

Query Match 100. Best Local Similarity 100. Matches 105; Conservative

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A APPLICATION NUMBER: 60/089600
BR FILING DATE: 1998-06-17
BA PELLICATION NUMBER: 60/089653
BR FILING DATE: 1998-06-17
BR APPLICATION NUMBER: 60/089801
BR FILING DATE: 1998-06-18
BR PLING DATE: 1998-06-18
BR PELING DATE: 1998-06-18
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BR PLING DATE: 1998-06-18
            R FILING DATE: 1998-06-04

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R APPLICATION NUMBER: 60/088029

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088030

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088033

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R APPLICATION NUMBER: 60/088212

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R FILING DATE: 1998-06-05

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R APPLICATION NUMBER: 60/089512
R FILING DATE: 1998-06-16
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R APPLICATION NUMBER: 60/089532
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R APPLICATION NUMBER: 60/08824
R FILING DATE: 1998-06-10
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R FILING DATE: 1998-06-11
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
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FFILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105
APPLICATION NUMBER: 60/089440
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-11
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: 0/06226
FRICH APPLICATION NUMBER: 60/06226
PRIOR APPLICATION NUMBER: 60/06216
PRIOR FILING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-12
PRIOR PRIOR MARE : 0/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PLING DATE: 1997-11-12
PRIOR PLING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/063312
PRIOR PLING DATE: 1998-03-20
PRIOR PLING DATE: 1998-03-20
PRIOR PLING DATE: 1998-04-28
PRIOR PLING DATE: 1998-04-28
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-03
PRIOR PLING DATE: 1998-06-03
PRIOR PLING DATE: 1998-06-03
PRIOR PLING DATE: 1998-06-03
PRIOR PLING DATE: 1998-06-04
PRIOR PLING DAT
                     Sequence 371, Application US/09989721
Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: ABKHENAZI, AVI J.
APPLICANT: BAKET, KEVIN P.
APPLICANT: BOTSTEIN, DAVID
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Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
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Eaton, Dan L.
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APPLICANT: Zhang, Zemin 1.

APPLICANT: Zhang, Zemin 1.

IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same 1. TITLE OF INVENTION: Acids Encoding the Same CURRENT PILID PROPRIED 1.1-14

PRICE APPLICATION NUMBER: US/09/992,598

CURRENT PILING DATE: 2001-11-14

PRICE APPLICATION NUMBER: 60/062260

PRICE APPLICATION NUMBER: 60/065186

PRICE APPLICATION NUMBER: 60/065186

PRICE PLING DATE: 1997-11-13

PRICE PLING DATE: 1997-11-13

PRICE APPLICATION NUMBER: 60/065311

PRICE APPLICATION NUMBER: 60/065311

PRICE APPLICATION NUMBER: 60/065310

PRICE PLING DATE: 1998-11-24

PRICE PLING DATE: 1998-01-25

PRICE PLING DATE: 1998-03-20

PRICE PLING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-05-28
PRIOR PELICATION NUMBER: 60/087607
PRIOR PELICATION NUMBER: 60/087609
PRIOR APPLICATION NUMBER: 60/087609
PRIOR PELING DATE: 1998-06-02
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PRIOR PILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
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PRIOR APPLICATION NUMBER: 60/088021
PRIOR PLING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-04
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Grimalodi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Goddard, Audrey
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                                                                                                                                                                                                                                                                                               Baker, Kevin P.
Botstein, David
                                                                                                                                                                                                                                                                                                                                                            Desnoyers, Luc
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                                                                                                                                          JS-09-992-598-371
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                                R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090254
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R PILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090696

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R APPLICATION NUMBER: 60/090862

R APPLICATION NUMBER: 60/090863

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R FILING DATE: 1998-06-26

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R APPLICATION NUMBER: 60/09186
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APPLICATION NUMBER: 60/090678
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APPLICATION NUMBER: 60/090690
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APPLICATION NUMBER: 60/091633
FILING DATE: 1998-07-02
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FILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/091544
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Gaps

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Indels

Length 105;

100.0%; Score 589; DB 9; 100.0%; Pred. No. 1.4e-53; 0; Mismatches

105; Conservative

Query Match Best Local Si Matches 105)

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Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                       Paoni, Nicholas F.
Gurney, Austin L.
                                     Cliavin, Ivar J.
                                                                   Napier, Mary A.
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Watenabe, Colin
APPLICANT: Watenabe, Colin
APPLICANT: Watenabe, Colin
APPLICANT: Wood, William I.
ITILE OF INVENTION: EG-VEGF NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: AND METHODS OF USE
FILE OF INVENTION: AND METHODS OF USE
CURRENT APPLICATION NUMBER: US 60/230, 978
PRIOR APPLICATION NUMBER: US 60/213, 637
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/115, 698
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/096,146
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
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APPLICANT: Ashkenazi, Avi J.
                                                            Sequence 2, Application US/09886242A Patent No. US20020172678A1 GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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Fong, Sherman
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Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-09-989-293A-371
                              US-09-886-242A-2
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US-09-886-242A-2
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
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PRIOR APPLICATION NUMBER: 60/090557
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PRIOR FILING DATE: 1988-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
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PRIOR PILING DATE: 1998-06-25
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PRIOR PILING DATE: 1998-06-25
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PRIOR PILING DATE: 1998-06-26
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PRIOR PILING DATE: 1998-07-07

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61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105 61 HPGSHKVPPFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105 δ

Search completed: September 20, 2005, 13:13:09 Job time : 170 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

September 20, 2005, 12:42:04; Search time 174 Seconds (without alignments) 309.013 Million cell updates/sec Run on:

US-10-692-299-2 589 1 MRGATRVSIMLLLVTVSDCA......CSRFPDGRYRCSMDLKNINF 105 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	D58294 homo ganien	рошо		_	Q863h4 bos taurus	P25687 dendroaspis	Q8jfq0 bombina max	Q8r413 rattus norv		Q9pw66 bombina var	Q9hc23 homo sapien	_		Q8jfe6 bombina max	Q8jfx8 bombina max	Q8jfy1 bombina max	Q8jfx9 bombina max	_	bombin	Q8uux3 gallus gall	արս արս	~	-			Q9qyz8 mus musculu	Q8bfw0 m mus muscu	O54908 mus musculu	Q80ul5 mus musculu	O43532 homo sapien	Q8n294 homo sapien
OI OI	PRK1 HIMAN	Iω	PRK1 RAT	Q8K4 <u>5</u> 7	Q863H4	VPRA_DENPO	Q8JFQ0	PRK2_RAT	Q863H5	BV8_BOMVA	PRK2_HUMAN	PRK2_MOUSE	Q6V8 <u>J</u> 7	Q8JFE6	QBJFXB	Q8JFY1	Q8JFX9	QBJFYO	Q8JFY2	Q8UUX3	Q8VEJ3	DKK4_HUMAN	DKK3_CHICK	Q9DDA4	DKK2_HUMAN	DKK2_MOUSE	QBBFWO	DKK1_MOUSE	Q80ULS	043532	Q8N294
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& Query Match	100.0	99.8	92.5	73.3	54.0	52.7	50.7	20.6	9.05	48.8	48.0	47.1	47.1	46.6	46.4	46.4	45.8	45.8	45.2	19.0	18.4	18	7	-	17.3	17.1	17.1	17.1	17.1	17.1	17.1
Score	589	288	545	432	318	310.5	298.5	298	298	287.5	282.5	277.5	277.5		273.5	273.5	269.5	269.5	266.5	112	108.5	107.5	107.5	104	102	101	101	101	101	100.5	100.5
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DKK3 HUMAN Q9ES33 DKK2 MOUSE DKK1, HUMAN Q6PVU5 G57464 Q6PQ81 Q9PWH3 CND0 MOUSE Q642A8 Q643A9	COL_RABIT P87363
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ALIGNMENTS

PRT; 105 AA. inted) transcation update) (Endocrine-gland-derived vascular endothelial (Mambakine) (UNQ600/PRO1186). transcation Vertebrata; Buteleostomi; tes; Catarrhini; Hominidae; Homo.	[1] SEQUENCE FROM N.A. MEDLINE=21160229; PubMed=11259612; Li M., Bullock C.M., Knauer D.J., Ehlert F.J., Zhou Q.Y.; Li M., Bullock C.M., Knauer D.J., Ehlert F.J., Zhou Q.Y.; Identification of two prokineticin cDNAs: recombinant proteins potently contract gastrointestinal smooth muscle."; Mol. Pharmacol. 59:692-698(2001). [2] SEQUENCE FROM N.A. MEDLINE=21419730; PubMed=11528470; DOI=10.1038/35091000; LeCouter J., Kowalski J., Foster J., Hass P., Zhang Z., Dillard-Telm L., Frantz G., Rangell L., DeGuzman L., Keller GA., Dillard-Telm L., Frantz G., Rangell L., DeGuzman L., Keller GA., midentification of an angiogenic mitogen selective for endocrine gland endothelium."; Nature 412:877-884(2001).	Fraser C.; "Mambakine, a snake venom related endocrine hormone that controls macrophages."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. [4] Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. [5] H. S. Gurney A.L., Abaya B., Baker K., Bakdwin D., Brush J., Clark H.F., Gurney A.L., Abaya B., Baker K., Bakdwin D., Brush J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Wandlen R., Watanabe C., Wiesand D., Woods K., Xie MH., Yansura D., Yi S., Yu G., Yuan J., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.; "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment." [5] Genome Res. 13:2265-2270(2003).
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STANDARD; 11. 40, Cr 11. 46, La 11. 46, La precursor (EG-VEGF) uman). zoa; Chor ria; Prim	Publication Public	Publ
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T. 1 PRAIL THUMAN STANDARD; PS8294; 16-OCT-2001 (Rel. 40, Las 16-OCT-2001 (Rel. 46, Las 25-JAN-2005 (Rel. 46, Las Prokineticin 1 precursor growth factor) (EG-VEGF) Name-BROKL; Homo sapiens (Human). Eukaryota; Metazoa; Chord Mammalia; Eutheria; Prima	[1] **SEQUENCE FROM N.A.* **MEDGINE=1116029; PubMed=11259612; *Li M., Bullock C.M., Knauer D.J., **Identification of two prokineticity **MEDGINETICAL CONTROL TO THE SEQUENCE FROM N.A. **MEDGINE=1419730; PubMed=11528470; **LeCouter J., Kowalski J., Foster J. **Dillard Telm L., Frantz G., Rangel **Dillard Telm L., Frantz G., Rangel **Pall F., Gurney A., Hillan K.J., **Identification of an anglogenic mendothellum."; **MEDGINETICAL TENTY G., Mendellum."; **MEDGINETICAL TEN	Fraser C.; Fraser C.; "Mambakine, a snake venom relat marcophages"; Submitted (APR-2001) to the EME [4] SEQUENCE FROM N.A. MEDLINE=22887296; Pubmed=129753 Clark H.F., Gurney A.L., Abaya Chen J., Chow B., Chul C., Crow Chen J., Chow B., Chul C., Crow Hang A., Kim H.S., Klimowski I. Lewis L., Liao D., Mark M., Roß Seshagiri S., Simmons L., Singh Vandlen R., Watanabe C., Wwiean Yi S., Yu G., Yuan J., Zhang M. Godowakk P., Gray A., "The secreted protein discovery effort to identify novel human bioinformatics assessment."; Genome Res. 13:2265-2270(2003).
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Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Ba Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,
Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
A Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Mitching M., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Generation and initial analysis of more than 15,000 full-length human
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10-0CT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Prokineticin 1 precursor (Endocrine-gland-derived vascular endothelial growth factor) (EG-VEGF).
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MEDLINES=2050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;

MEDLINES=2050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;

Madda Y., Takatsu Y., Takatsu Y., Kumano S., Ishibashi Y., Suenaga M., Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S., Inatoni N., Ohtaki T., Onda H., Fujino M.;

"Isolation and identification of EG-VEGF/prokineticins as cognate ligands for two orphan G-protein-coupled receptors.";

Biochem Biophys. Res. Commun. 293:396-402(2002).

"Induces proliferation, migration and fenestration (the formation of membrane discontinuities) in capillary endothelial cells derived from endocrine glands. Has little or no effect on a variety of other endothelial and non-endothelial cell types (By
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 105 AA; 11729 MW; E570FDE30EFB52D2 CRC64;
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                                                                                                                                     Protein Sci. 13:2819-2824(2004).

-I- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle. Induces proliferation, migration and fenestration (the formation of membrane discontinuities) in capillary endothelial cells derived from endocrine glands. Has little or no effect on a variety of other endothelial and non-endothelial cell types.
-I- SUBCELIULAR LOCATION: Secreted.
-I- TISSUE SPECIFICITY: Expressed in the steroidogenic glands, ovary, testis, adrenal and placenta.
-I- SIMILARITY: Belongs to the prokinecitin family.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                             peptide prediction based on analysis of experimentally
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Pfam; PF06607; Prokineticin; 1.
Direct protein sequencing; Growth factor; Mitogen; Signal.
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              PubMed=15340161; DOI=10.1110/ps.04682504;
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EMBL; AY029225; AAK33111.1; -.
EMBL; AX358683; AAQ89046.1; -.
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                   verified cleavage sites."
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Matches 105; Conservative
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Query Match

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DT 01-7
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CO Buka
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PRELIMINARY;
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                                                                                                                                                                                                                                                    Bos taurus (Bovine).
                       Best Local Similarity
Matches 71; Conserv
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                   Bovinae, Bos
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              Query Match
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                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                        1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC 60
                                                                                                                                                                                                                                                                                                                                                       1 MRGAVQVFIMLLLATVSDCAVITGACERDVQCGAGTCCAISLWLRGLRLCTPLGREGEEC 60
                                                                                                                                                                                                                                                                                                                     Gaps
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MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
Weaver D.R., Leslie F.M., Zhou Q.Y.;
"Prokineticin 2 transmits the behavioural circadian rhythm of the
suprachiasmatic nucleus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0005576; C:extracellular; IDA.
GO:000187; P:activation of MAPK; IDA.
GO:0007623; P:circadian rhythm; TAS.
GO:0008284; P:postitive regulation of cell proliferation; IDA.
GO:0045765; P:regulation of angiogenesis; IDA.
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6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                   HPGSHKIPFFRKRQHHTCPCSPSLLCSRFPDGRYRCSQDLKNVF 105
                                                                                                                                                                                                                                                                       8DF0C42122B1C5B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 AA; 9192 MW; 7BBE3EC6B16A8011 CRC64;
          SIMILARITY: Belongs to the prokinecitin family.
SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                               By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
                                                                                                                                                                                            Potential.
Prokineticin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
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                                                                                                                    EMBL; AY089983; AAM09104.1; -.
HSSP; P25687; 11MT.
RGD; 620898; Proxl.
InterPro; IPR009523; Proxineticin.
Pfam; PF06607; Proxineticin; 1.
Growth factor; Mitogen; Signal.
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Pfam; PF06607; Prokineticin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 417:405-410(2002).
EMBL; AF487281; AAM49573.1; -.
HSSP; P25687; 11MT.
                                                                                                                                                                                                                                                                       11642 MW;
                                                                                                                                                                                                                                                                                              92.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Prok1; Synonyms=Pk1;
                                                                                                                                                                                                                                                                                                                    94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prokineticin 1 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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38
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78
86
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26
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105 AA;
                                                                                                                                                                                                                                                                                                        Similarity
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DISULFID
* SEQUENCE
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SEQUENCE
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                                                                                                                25 ACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCPCLPNL
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Joubert F.J., Strydom D.J.;
"Snake venom. The amino acid sequence of protein A from Dendroaspis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1992 (Rel. 22, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Intestinal toxin 1 (MIT 1) (MIT1) (Venom protein A).
Dendroaspis polylepis polylepis (Black mamba).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Testis;
BEDLINE-25612805; PubMed=12728244; DOI=10.1038/sj.embor.embor830;
Kaser A., WithImayr M., Lepperdinger G., Kreil G.;
"The AVIT protein family.";
EMBO Rep. 4:469-473(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleoetomi,
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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54.0%; Score 318; DB 2; Length 108;
Best Local Similarity 51.9%; Pred. No. 1e-24;
Matches 54; Conservative 15; Mismatches 27; Indels
Score 432; DB 2; Length 81; Pred. No. 2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 LGREGEECHPGSHKVPFFRKKKKHHTCPCLPNLLCSRFPDGRYRC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF06607; Prokineticin; 1.
SEQUENCE 108 AA; 11672 MW; C00410399A9B215E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Bv8/prokineticin 2-like protein splice variant.
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                                                        5; Mismatches
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                                                                                                                                                                                                                              LCSRFPDGRYRCSMDLKNINF 105
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                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                            Elapidae; Elapinae; Dendroaspis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AY192558; AAP31907.1; -. HSSP; P25687; 11MT.
  73.3%;
87.7%;
                                                        Conservative
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Query Match
Best Local Similarity
Matches 52; Conserv
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620280; Bv8.
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Q8R413;
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A Boisbouvier J., Albrand J.-P., Blackledge M., Jaquinod M.,
Schweitz H., Lazdunski M., Marion D.;
Schweitz H., Lazdunski M., Marion D.;
Schweitz H., Lazdunski M., Marion D.;
T. A structural homologue of colipase in black mamba venom revealed by
II Mal 1981.205-219(1998).
C. I. Mol. 1801.205.219(1998).
C. I. SUBCELDULAR LOCATION: Secreted.
C. I. SUBCELDULAR LOCATION: SECRETION: SECR
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                                                                                           MEDILINE=20036442; PubMed=10567694; DOI=10.1016/S0014-5793(99)01459-3; Schweitz H., Pascaud P., Diochot S., Moinier D., Lazdunski M.; "MITI, a black mamba toxin with a new and highly potent activity on intestinal contraction."; PEBS Lett. 461:183-188(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB-Skin secretions;
MEDLINE-22515712; PubMed-12628381; DOI-10.1016/S1096-4959(02)00294-4;
Lai R., Liu H., Lee W.H., Zhang Y.;
"Two novel Bv8-like peptides from skin secretions of the toad Bombina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina. NCBI_TaxID=161274;
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Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad)
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SEQUENCE 96 AA; 10198 MW; EC4BAA5EFE49B2F0 CRC64;
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C -> S (in Ref. 1).
S -> C (in Ref. 1).
   Hoppe-Seyler's Z. Physiol. Chem. 361:1787-1794(1980)
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:ive 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 AA;
                                                                           CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
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QQUFQO
ID QQUF
AC QQUF
DT 01-0
DT 01-0
DT 01-0
DT 01-M
DE BV8
OC BUKA
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                                               ä
                                                                                                              -!- FUNCTION: May function as an output molecule from the suprachiaematic nucleus (SCM) that transmits behavioral circadian rhythm. May also functionally within the SCN to synchronize output. Potently contracts gastrointestinal (GI) smooth muscle (By output.
                                                                                     1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M., Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S., Inatoni N., Ohtaki T., Onda H., Prijino M. "Isolation and identification of EG-VEGF/prokineticins as cognate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague-Dawley;
MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;

similarity).
SUBCELLULAR LOCATION: Secreted (By similarity).
SUBCELLULAR LOCATION: Expressed at high levels in testis and at lower levels in brain, lung, ovary, spleen, thymus and uterus.
INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light; inhibited by period genes (ERR1, PER2 and PER3) and cryptochrome genes (CRY1 and CRY2) (Probable).
SIMILARITY: Belongs to the prokinecitin family.

                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-22022134; PubMed-12024266; DOI=10.1038/417405a; Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J., Weaver D.R., Leelie F.M., Zhou Q.-Y.; "Prokineticin 2 transmits the behavioural circadian rhythm of the suprachiaematic nucleus:"; Nature 417:405-410(2002).
                                               ï
      Length 96;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ligands for two orphan G-protein-coupled receptors.";
Biochem. Biophys. Res. Commun. 293:396-402(2002).
                                                                                                                                                                                                     61 HPASHKVPYNGKRLSSLCPCKSGLTCSKSGE-KFQCS 96
                                                                                                                                                                          61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCS 97
50.7%; Score 298.5; DB 353.6%; Pred. No. 8.8e-23; tive 16; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                       28-FEE-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential.
Prokineticin 2.
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Pfam; PF06607; Prokineticin; 1.
Biological rhythms; Neuropeptide; Signal.
SIGNAL 27 107 Prokineticin
CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFFECT ON CIRCADIAN LOCOMOTOR ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AY089984; AAM09105.1; -. HSSP; P25687; 11MT.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (PK2)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Prokineticin 2 precursor
Name=Prok2; Synonyms=Bv8;
Rattus norvegicus (Rat).
                                               52; Conservative
                                                                                                                                                                                                                                                                                                                                 STANDARD;
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19
96
38
50
78
86
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es 49; Conserv
  121 RYTC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 AA;
                                                                                                                                                                   NCBI_TaxID=8348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRK2 HUMAN
                                                           BV8_BOMVA
Q9PW66;
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                                     RESULT 10
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RG; GO:0001664; F:G-protein-coupled receptor binding; ISS.

RG; GO:0001525; P:angiogenesis; ISS.

RG; GO:0001525; P:angiogenesis; ISS.

RG; GO:0001525; P:anti-apoptosis; ISS.

RG; GO:0001525; P:chemotaxis; ISS.

RG; GO:0007204; P:chemotaxis; ISS.

RG; GO:0007104; P:cytosolic calcium ion concentration elevation; ISS.

RG; GO:0007104; P:cytosolic calcium ion concentration elevation; ISS.

RG; GO:0007104; P:cytosolic calcium ion concentration elevation; ISS.

RG; GO:0007105; P:cytosolic calcium ion concentration elevation; ISS.

RG; GO:0007105; P:cytosolic calcium ion concentration elevation; ISS.

RG; GO:0007204; P:protein coupled receptor protein signalin. .; ISS.

RG; GO:0007204; P:protein of pain; ISS.

RG; GO:0007204; P:protein equation of smooth muscle contra. .; ISS.

RG; GO:0007204; P:protein elevation; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                       96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 LGREGEECHPGSH-------KVPFFRKRKHHTCPCLPNLLCSRFPDG 92
                                                                                                                                             1 MRGATRVSIMLLLV-----TVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTP
                                                                                                                                10 MLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22612805; PubMed=12728244; DOI=10.1038/sj.embor.embor830; Kaser A., Winklmayr M., Lepperdinger G., Krell G.; "The AVIT protein family."; EMBO Rep. 4:469-473(2003).
EMBL; AY192557; AAP31906.1; -.
                                                                                                          ö
                                                                                50.6%; Score 298; DB 1; Length 107; 54.0%; Pred. No. 1.1e-22; tive 16; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 128;
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
W, BDFF316CDCB5FED0 CRC64;
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                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Bv8/prokineticin 2-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.6%; Score 298; DB 2; 43.5%; Pred. No. 1.3e-22; iive 15; Mismatches 27;
                                                                                                                                                                                                                                                                 128 AA.
                                                                                                                                                                                            70 FRKRKHHTCPCLPNLLCSRFPDGRYRC 96
                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                PRT;
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SEQUENCE 128 AA; 14290 MW;
 45
57
85
85
87
87
87
87
103
89
11594 MW;
                                                                                            llarity 54.0%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Conservative
                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
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Best Local Similarity
 33
39
44
67
87
107 AA;
                                                                                            Local Similarity
tes 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Testis;
DISULPID
                      DISULPID
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                                               DISULFID
                                                           SEQUENCE
                                                                                 Query Match
                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99349621; PubMed=10422759; DOI=10.1016/S0014-2999(99)00229-0; Mollay C., Wechselberger C., Mignogna G., Negri L., Melchiorri P., Barra D., Kreil G.;
                                                                                                                                Protein By8 precursor.
Bombina variegata (Yellow-bellied toad).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Bv8, a small protein from frog skin and its homologue from snake venom induce hyperalgesia in rats.";
Bur. J. Pharmacol. 374:198-196(1999).
-i- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity.
By similarity.
By similarity.
By similarity.
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A12490A7437609B4 CRC64;
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25-JAN-2005 (Rel. 46, Last annotation update)
Prokinetion 2 preursor (PK2) (Protein Bv8 homolog)
Name=PROK2; Synonyms=BV8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Induces hyperalgesia.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the prokinecitin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCS
                                                                              16-OCT-2001 (Rel. 40, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
96 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 AA
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE-Skin secretion;
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR009523; Prokineticin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF06607; Prokineticin.
Direct protein sequencing; Signal.
SIGNAL 19
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HSSP; P25687; 11MT.
                                                    16-OCT-2001 (Rel. 40, Created)
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10102 MW;
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G0:0005576; C:extracellular; TAS.
G0:0001664; F:G-protein-coupled receptor binding; TAS.
G0:0001167; P:activation of MAPK; TAS.
G0:0001252; P:angiogenesis; IDA.
G0:0005216; P:anti-apoptosis; IDA.
G0:0008281; P:cell proliferation; IDA.
G0:0007204; P:cytosolic calcium ion concentration elevation; TAS.
G0:0007204; P:cytosolic calcium ion concentration elevation; TAS.
G0:0007204; P:cytosolic calcium ion concentration elevation; TAS.
G0:000531; P:protein coupled receptor protein signalin. .; NAS.
G0:0005931; P:proteption of pain; TAS.
G0:0019333; P:perception of pain; TAS.
G0:0012831; P:perception of pain; TAS.
G0:0007281; P:positive regulation of smooth muscle contra. .; IDA.
G0:0007281; P:positive regulation of smooth muscle contra. .; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOId=Q9HC23-2; Sequence=VSP 005219;
TISSUE SPECIFICITY: Expressed in the testis and, at low levels, in
                                                                                                                                                                                                                                                                                                                                                                               PubMed=15340161; DOI=10.1110/ps.04682504;
PubMed=15340161; DOI=10.1110/ps.04682504;
PubMed=15340161; DOI=10.1110/ps.04682504;
Panga 2., Henzel W.J.;
Signal peptide prediction based on analysis of experimentally verified cleavage sites.";
Protein Sci. 13:2819-2824(2004).
-!- FUNCION: May function as an output molecule from the suprachiasmetic nucleus (SCN) that transmits behavioral circadian rhythm. May also function locally within the SCN to synchronize output. Potently contracts gastrointestinal (GI) smooth muscle.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                 MEDLINE=20047850; PubMed=10580115; DOI=10.1016/S0014-5793(99)01473-8; Wechselberger C., Puglisi R., Lepperdinger G., Boitani C., Kreil G.; "The mammalian homologue of Bv8 from frog skin is mainly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the small intestine. INDUCTION: Activated by CLOCK and BWAL1 heterodimers and light; inhibited by period genes (PER1, PER2 and PER3) and cryptochrome genes (CRX1 and CRX2) (Probable). SIMILARITY: Belongs to the prokinecitin family.
                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=21160229; PubMed=11259612;
Li M., Bullock C.M., Knauer D.J., Ehlert F.J., Zhou Q.-Y.;
"Identification of two prokinetricin cDNAs: recombinant proteins
potently contract gastrointestinal smooth muscle.";
Mol. Pharmacol. 59:692-698(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=09HC23-1; Sequence=Displayed;
                                                                                         SEQUENCE OF 5-129 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                             FEBS Lett. 462:177-181(1999).
Homo sapiens (Human)
                                                     NCBI_TaxID=9606;
                                                                                                                                                                                           spermatocytes.";
                                                                                                                 rissum=Testis;
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STRAIN=C57BL/6J; TISSUE=Testis;
STRAIN=22354683; Dubde=1246681;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Golobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 LLLTPRAGDAAVITGACDKDSQCGGGACCAVSIWVKSIRICTPMGKLGDSCHPLTRKNNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=129/SvJ;
PubMed=11054548; DOI=10.1016/S0378-1119(00)00355-3;
Jilek A., Engel B., Beier D., Lepperdinger G.;
"Murine Bv8 gene maps near a synteny breakpoint of mouse chromosome 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20047850; PubMed=10580115; DOI=10.1016/S0014-5793(99)01473-8;
                                                                                                                                                                                                                                                                                                                                                                                                           21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-22022134; PubMed=12024206; DOI=10.1038/417405a; Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J., Weaver D.R., Leslie F.M., Zhou Q.-Y.; "Prokineticin 2 transmits the behavioural circadian rhythm of the suprachiaematic nucleus."; Nature 417:405-410(2002)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wechselberger C., Puglisi R., Lepperdinger G., Boitani C., Kreil G. "The mammalian homologue of Bv8 from frog skin is mainly expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                    Length 129;
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                                                                                  By similarity.
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By similarity.
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A similarity.
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16-OCT-2010 (Rel. 40, Created)
16-OCT-2010 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Prokineticin 2 precursor (PK2) (Protein Bv8 homolog)
Name=Prok; Synonyms=Bv8;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                 Score 282.5; DB Pred. No. 5e-21;
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                                                         Prokineticin 2
                                                                                                                                                                                                                                                                                                                                                                                                              15; Mismatches
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Best Local Similarity 44.4%
Matches 48; Conservative
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129
46
58
107
115
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Neuropeptide; Signal.
                                                                                                                                                                                                                                                                                           129 AA;
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Gasterland T.A., Fletcher C.F., Forrest A., Frazer K.S.,
Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Grimmond S., Gustinacich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
A Grimmond S., Gustinacich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
A Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
A Majott D.R., Mattais L., Marchionni L., McKenzie L., Miki H.,
A Majott D.R., Mattais L., Marchionni L., McKenzie L., Miki H.,
A Majott D.R., Mattais E., Marchionni L., McKenzie L., Miki H.,
A Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
A Wilming L.G., Wynshaw-Boris A., Vanagisawa M., Vang I., Vang L.,
Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Pukuda S.,
A Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Mattai A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Mattai A., Nathi L., Lander E.S., Rogers J.,
Mattai A., Nathi L., Rayashizaki Y.,
Mathalyais of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: Expressed in the SCN and among a few other discrete brain areas, including the islands of Calleja, media 1 peroptic area of the hypothalamus and the shell of the mucleus accumbens. Highly expressed in testis. In the SCN, expression subjected to high amplitude of circadian oscillation.
BEVELOPMENTAL STAGE: Expressed in mid-late pachytene spermatocytes at the stages VII, VIII and IX of the semiferous epithelial cycle. INDUCTION: Activated by CLOCK and BNAL1 heterodimers and light; inhibited by period genes (PER1, PER2 and PER3) and cryptochrome SIMILARITY: Belongs to the prokinecitin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: May function as an output molecule from the suprachiasmatic nucleus (SCN) that transmits behavioral circadian thythm. May also function locally within the SCN to synchronize output. Potently contracts gastrointestinal (GI) smooth muscle (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0005576; C:extracellular; ISS.
GO:0001664; F:G-protein-coupled receptor binding; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLUIAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
Event=Alternative_splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9QXU7-2; Sequence=VSP_005220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q9QXU7-1; Sequence=Displayed;
Name=2; Synonyms=Bv8-b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF182066, AAF15261.1;
EMBL, AF182066, AAC09439.1;
EMBL, AF182067, AAG09439.1;
EMBL, AF487280, AAM49572.1;
EMBL, AKO18462, BAB29857.1;
HSSP, P25687, 11mT.
MGD, MGI:1354178; Prok2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF182064; AAF15259.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 420:563-573(2002)
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GO:0000187; P:activation of MAPK; ISS. GO:0001525; P:angiogenesis; ISS. GO:0006916; P:anti-apoptosis; ISS. GO:0008283; P:cell proliferation; ISS. GO:0006935; P:chemotaxis; ISS.

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62 QVGDSCHPLTRKSHVANGRQERRRAKRRKKKKKVFPWGRRMHTTCPCLPGLACLRTSFNR 121
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GO; GO:0007204; P:cytosolic calcium ion concentration elevation; ISS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; ISS.
GO; GO:0006954; P:inflammatory response; ISS.
GO; GO:0019233; P:perception of pain; ISS.
GO; GO:0019233; P:perception of pain; ISS.
GO; GO:0007283; P:spermatogenesis; ISS.
InterPro; IRR009523; Prokineticin.
Pfam; PF06607; Prokineticin; 1.
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                                                                                                                                                                                                  By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
Missing (in isoform 2).
ATIGH VSP 005220.
SHVANGRQERRAKRRKRKEVPFWGRRMHTCPCLPGLAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GDPRCAPLILILILPILFTPPAGDAAVITGACDKDSQCGGGMCCAVSIWVKSIRICTPWG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Gaps
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STRAIN-Sprague-Dawley;
Chen J., Survenberg T.W., Liu C.;
Chen J., Gutte. S., Kuei C., Wilson S.J., Lovenberg T.W., Liu C.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY348322; AAR06924.1; -..
EMBL; AY348322; Prokineticin.
Procept PF06607; Prokineticin.
SEQUENCE 128 AA; 14223 MW; 67050CC1A7D59466 CRC64;
                                                                                                                                                                                                                                                                                                                                      LRTSFNRFICLARK -> VSVCTGILGVPSH (in
                                                                                                                                              Alternative splicing Biological rhythms; Neuropeptide; Signal.
SIGNAL
SIGNAL
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SIGNAL
1 26 Potential.
CHAIN 27 128 Proxincticin 2.
DISULPID 39 57 By similarity.
DISULPID 44 106 By similarity.
DISULPID 108 124 By similarity.
DISULPID 108 124 By similarity.
Missing in isoform 2).
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43.5%; Pred. No. 1.6e-20;
ive 16; Mismatches 24; Indels 21.
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128 AA; 14185 MW; 5F08BA177FDDB58C CRC64;
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Last annotation update)
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40.7%; Pred. No. 1.6e-20;
ative 19; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                         isoform 3)
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les 47; Conservative 1
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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Matches
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Search completed: September 20, 2005, 12:58:58
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TISSUE-Skin secretions;
MEDLINE=22515712; PubMed=12628381; DOI=10.1016/S1096-4959(02)00294-4;
Lai R., Liu H., Lee W.H., Zhang Y.;
"Two novel Bv8-like peptides from skin secretions of the toad Bombina maxima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM8-f protein precursor.

Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Amphibia, Batrachia, Anura, Archeobatrachia, Bombinatoridae, Bombina.

NCBI_TaxID=161274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                         01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
BM8-a protein precursor (Bv8 protein homolog 1).
Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
Bukaryota; Metazoa; Chordeta; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen T., Farragher S., Bjourson A.J., Orr D.F., Rao P., Shaw C., "Granular gland transcriptomes in stimulated amphibian skin secretions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 134:509-514(2003).
EMBL; AJ440230; CAD29340.1; -.
EMBL; AP411090; AAN03821.1; -.
HSSP; P25687; IIMT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen T., Farragher S., Bjourson A.J., Orr D.F., Rao P., Shaw C., "Granular gland transcriptomes in stimulated amphibian skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                          77 ANGRQERRRAKRRKKEVPFWGRRMHTTCPCLPGLACLRTSFNRFIC 124
------VPFFRKRKHHTCPCLPNLLCSRFPDGRYRC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch
1 Similarity 49.5%; Pred. No. 2.4e-20;
48; Conservative 17; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 19 Potential.
20 96 BM8-a protein.
96 AA; 10117 MW; 2269AAC8654B18A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPASHKVPYNGKRLSSLCPCNTGLTCSKSGE-KFQCS 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCS 97
                                                                                                                                                                                               96 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ą
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                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro, IPR009523; Prokineticin.
Pfam; PF06607; Prokineticin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biochem. 371:125-130(2003)
[2]
                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=161274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Skin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OBJFX8
                                                                                                                                 RESULT 14
C86JFE6
C96JFE6
DT 01-0C
DT 0
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Matches
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1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                             1;
                                                                                                                                                                           DB 2; Length 96;
                                                                                                                                                                                                             32; Indels
                                                                                                     Potential.
BM8-f protein.
2269A070FFEI18A6 CRC64;
                                                                                                                                                                                                                                                                                                                                       61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCS 97
                                                                                                                                                                           46.4%; Score 273.5; DB 250.5%; Pred. No. 3.1e-20;
                                                                                                                                                                                                             15; Mismatches
J. Biochem. 371:125-130(2003).
BMEL; AJ40235; C. AD202345.1; -.
HSSP. P25687; IMT.
InterPro; IPR009523; Prokineticin.
                                                                                                        1 19 E
20 96 E
96 AA; 10058 MW;
                                                     InterPro; IPR009523; Prokinet
Pfam; PF06607; Prokineticin;
Signal.
SIGNAL.
                                                                                                                                                                                           Local Similarity 50.5
Les 49; Conservative
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ï 9 9

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
               Copyright
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OM protein - protein search, using sw model

September 20, 2005, 12:43:34; Search time 39 Seconds (without alignments) 259.045 Million cell updates/sec Run on:

Title: Perfect score:

US-10-692-299-2 589 1 MRGATRVSIMLLLVTVSDCA......CSRFPDGRYRCSMDLKNINF 105 Sequence:

Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	REIC protein - hum	protein -	hetical pr	E C	colipase precursor		cysteine-rich prot	MEGF6 protein - ra	fertillin beta cha	notch 3 protein -	notch homolog - se	colipase precursor	hypothetical prote	tumor necrosis fac	laminin alpha-1 ch	hypothetical prote	fibrillin I - bovi	fibrillin 1 precur	laminin gamma-1 ch	acrogranin - guine	fibulin 1 precurso	fibulin 1 precurso	thrombospondin pre	hypothetical prote	collagen, cuticula	granulin precursor	probable vitelloge	fibrillin-1 precur	hypothetical prote
SUMMARIES	QI	JC7188	T08179	T16840	T09059	хгно	A56175	A55035	T13954	JC4861	S45306	T31070	151909	T27283	A35356	S14458	T25473	A55567	A47221	MMFFB2	148141	B36346	C36346	A39804	T13576	S34665	GYHU	T18308	A55624	T24293
	80	7	~	7	~	-	7	7	7	7	7	~	~	~	Н	7	~	7	7	-	7	~	~	-	~	~	-4	~	~	7
	Query Match Length	350			٦				1574		2318			_		ო					591	601	683	1178	1854	286	593	1847	2871	802
di	Query	17.1	15.0	14.1	13.8	13.4	13.2	13.1	12.8	12.7	12.7	12.7	12.6	12.6	12.4	12.4	12.3	12.3	12.3	12.2	12.1	12.1	12.1	12.1	12.1	12.1	12.1	12.0	12.0	11.8
	Score	100.5	88.5	83	81	79	77.5	77	75.5	75	75	75	74	74	73	73	72.5	72.5	72.5	72	71.5	71.5	71.5	71.5	71.5	71	71	70.5	70.5	69.5
	Result No.		8	e	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	Notch homolog prot	alpha-2-macroglobu	fibrillin-2 precur	hemocytin - silkwo	laminin alpha-1 ch	C-Delta-1 - chicke	serine/threonine k	hypothetical prote	thrombospondin 2 p	osteonidogen - hum	colipase precursor	hypothetical prote	hypothetical prote	nerve growth facto	mannosyl-oligosacc
T24294	T30201	825111	A54105	S52093	S18253	150719	T14450	T18649	A42587	G00043	A46717	T25138	T25137	GOHON	A33901
N	~	Н	N	N	N	N	N	~	~	N	~	~	~	Н	7
949	2352	4545	2918	3133	3712	728	850	,884	1172	1376	112	345	358	427	547
11.8	11.8	11.8	11.7	11.7	11.7	11.6	11.6	11.6	11.6	11.6	11.5	11.5	11.5	11.5	11.5
69.5	69.5	69.5	69	69	69	68.5	68.5	68.5	68.5	68.5	68	68	68	68	89
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1
	JC7188
	RBIC protein - human
	C;Species: Homo sapiens (man)
	C;Date: 04-Mar-2000 #sequence revision 04-Mar-2000 #text change 11-May-2000
	C;Accession: JC7188
_	R;Tsugi, T.; Miyazaki, M.; Sakaguchi, M.; Inoue, Y.; Namba, M.
	Biochem. Biophys. Res. Commun. 268, 20-24, 2000
	A; Title: A REIC gene shows down-regulation in human immortalized cells and human tumor-de
	A; Reference number: JC7188; MUID:20119095; PMID:10652205
	A;Accession: JC7188
	A; Molecule type: mRNA
	A;Residues: 1-350 <tsu></tsu>
	A;Cross-references: DDBJ:AB034203
	A;Experimental source: heart
	C; Comment: This protein is a secreted glycoprotein for head induction in amphibian embryc
	C;Genetics:
	A;Gene: reic
	C; Superfamily: human REIC protein
	C; Keywords: cardiac muscle; coiled coil; glycoprotein; heart; tumor
	Query Match 17.1%; Score 100.5; DB 2; Length 350;
_	Best Local Similarity 37.7%; Pred. No. 0.0089;
	Matches 26; Conservative 3; Mismatches 29; Indels 11; Gaps 4;
	Qy 26 ÇERDVQÇGAĞTÇÇALSLMLRGLRMCTPLGREGEECH-PGŞHKVPPFRKRKHHT 77

쉽

78 CPCLPNLLC 86 ò

265 CPCASGLLC 273 g

LRG5 protein - Chlamydomonas reinhardtii
C;Species: To S179
R;Gloeckner, G.; Beck, C.F.
submitted to the RMEL Data Library, October 1996
R;Gloeckner, G.; Beck, C.F.
submitted to the RMEL Data Library, October 1996
A;Secession: T08179
A;Pecession: T08179
A;Accession: T08179
A;Accession: T08179
A;Accession: T08179
A;Accession: T08179
A;Accession: T08179
A;Residues: periminary; translated from GB/EMBL/DDBJ
A;Residues: 1-640 <GLO>
A;Cross-references: UNIPROT:Q96397; EMBL:U73817; NID:g1644369; PID:g1644370
A;Genetics:
A;Genetics:

us-10-692-299-2.rpr

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A, Cross-references: GDB:127277; OMIM:120105
A, Map position: 6pter-6p21.1
                                                                                                                                                                                                                                                                                                                                                                                colipase precursor [validated] - human
                                                                                                                                                                                                                                                               234 ACPPGSCLNGGTCQLVPEG 252
                                                                                                                                                                                                                77 TCP---CLPNLLCSRFPDG 92
                      Query Match
Best Local Similarity 30.4%;
Matches 24; Conservative
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Best Local Similarity 28.4%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: procolipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 IMLLLVTVSDCAVITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 23-108 <STE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-112 <SIM>
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A; Residues: 1-112 < LOW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: A33949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: GDB: CLPS
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A;Molecule type: DNA
A;Residues: 1-1101 <GEI>
A;Residues: 1-1101 <GEI>
A;Cross-references: UNIPROT:Q22378; EMBL:U39644; NID:g1049339; PID:g1049343; PIDN:AAA803
A;Experimental source: strain Bristol N2
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Acces: In: Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Acces: In: T09059
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Submitted to the EMBL. Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region. A;Reference number: 216543
A;Accession: T09059
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1964 RDW>
A;Residues: 1-1964 RDW>
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A Map position: 17
A Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 1679/3; 1729/1; 1761/3
C Superfamily: notch protein; ankyrin repeat homology; EGF homology
C Keywords: receptor; signal transduction
F;514-545/Domain: EGF homology < EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
                                                                                             32 CGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCPCLPNLLCSRF-- 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P31695; EMBL:AF030001; NID:g2564945; PID:g2564947 C;Genetics:
                                                                                                                                                                                                                                                                                                             nypothetical protein T10E10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16840
R;Geisel, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 -- LRMCTPLGR-----BGEECHPG-----SHKVPFFRKRKHHTCPCLPNLLCS
                                                 Gaps
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                                              23;
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  Length 640;
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                                              24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Geisel, C.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid T10E10.
A;Reference number: Z18588
Score 88.5; DB 2;
Pred. No. 0.24;
5; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 83; DB 2
Pred. No. 1.3;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 LVTVSDCAVITGACERDVQCGAGTCCAISLWLRG
                                                                                                                                                                                                                     | ||:|||:
534 RWRCGWAPGGRWRCSL 549
Query Match
Best Local Similarity 31.6%;
Matches 24; Conservative
                                                                                                                                                                                          -----PDGRYRCSM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.1%;
24.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T16840
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Risims, H.F.; Lowe, M.E.
Biochemistry 31, 7120-7125, 1992
A;Title: The human colipase gene: isolation, chromosomal location, and tissue-specific e)
A;Reference number: A42568; MUID:92353041; PMID:1643046
A;Recession: A42568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P04118; GB:M95529; NID:g180842; PIDN:AAB05818.1; PID:g1483624
A;Cross-references: UNIPROT:P04118; GB:M95529; NID:g180842; PIDN:AAB05818.1; PID:g1483624
A;Note: sequence extracted from NCBI backbone (NCBIN:110576, NCBIN:110578, NCBIP:110580)
B;Cowe, M.B.; Rosenblum, J.L.; McEwen, P.; Strauss, A.W.
Biochemistry 29, 823-828, 1399,
Biochemistry 29, 823-828, 1399
A;Title: Cloning and characterization of the human colipase cDNA.
A;Reference number: A33949; MUID:90248429; PMID:2337598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Comment: Colipase, a cofactor of triacylglycerol lipase (EC 3.1.1.3), forms a 1:1 stoic se the enzyme is washed off by bile salts, which are known to have an inhibitory effect c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 28/3; 69/3
C; Superfamily: Colipase
C; Superfamily: Colipase
C; Superdamily: Colipase
C; Superdamily: Colipase
F;1-17/Domain: signal sequence #status predicted <SIG>F;1-17/Domain: signal sequence #status predicted <SIG>F;18-22/Domain: amino-terminal propeptide #status predicted <APP>F;23-108/Product: colipase #status experimental <AMT>F;19-112/Domain: carboxyl-terminal propeptide #status predicted <CPP>F;34-104,40-56,44-80,45-78,66-86/Disulfide bonds: #status predicted
F;69,72,75,76/Binding site: micellar substrate (Lys, Tyr, Tyr, Tyr) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               œ,
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A;Note: evidence of partial N-g1ycosylation, possibly at Asn-43
R;Sternby, B.; Engetrom, A.; Hellman, U.; Vihert, A.M.; Sternby, N.H.; Borgstrom,
Biochim. Biophys. Acta 784, 75-80, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                          188 CERDINECFLEPGPCPOGTSCHNTL---GSYQCLCPVGQEGPQC-----KLRKG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                 26 CERDVQ-----CGAGTCCAISLWLRGLRMC-TPLGREGEECHPGSHKVPFFRKRKHH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .Species: Homo saplens (man)
.Date: 04-Dec-1986 #sequence revision 19-May-1995 #text_change 09-Jul-2004
.Accession: A42568; A33949; A03163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --ACERDVQCGAGTCCAISLWLRGLRMCTPLGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 NSEC---SVKTLY---GIYYKCPCERGLTC----EGDKTIVGSITNTNF 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 GEECHPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
DB 2; Length 1964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 79; DB 1; Length 112;
Pred. No. 0.5;
9; Mismatches 45; Indels
Score 81; DB 2; Length 196
Pred. No. 3.4;
7; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 784, 75-80, 1984
A; Title: The primary sequence of human pancreatic colipase.
A; Reference number: A90652, MUID:84104937; PMID:6691986
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A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs the Akeference number: 214126; MUID:98360089; PMID:9693030 A;Accession: T13954 A;Accession: T13954 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-1574 <NAK>
A;Cross-references: UNIPROT:088281; EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: UNIPROT: Q99965; GB: U38805; NID: 94151118; PIDN: AAD04206.1; PID: 94151113 C; Comment: This protein is an integral sperm membrane glycoprotein, and plays a role in £ C; Superfamily: mouse meltrin alpha; disintegrin homology C; Superfamily: mouse meltrin alpha; transmembrane protein C; Keywords: glycoprotein; integrin binding; transmembrane protein F: 382-734/Product: fertillin beta chain #status predicted <NAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          notch 3 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Reb-1995 #sequence_revision 20-Reb-1995 #text_change 09-Jul-2004
C;Accession: S45306
R;Lardelli, M.; Dahlstrand, J.; Lendahl, U.
Mech. Dev. 46, 123-136, 1994
A;Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-1A;Reference number: S45306; MUID:95001556; PMID:7918097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F.382-467/Domain: disintegrin homology <DIS>
F.48450/Fegjon: integrin binding #status predicted
F.566-708/Domain: transmembrane #status predicted <TMM>
F.566-708/Domain: transmembrane #status predicted <TMM>
F.121,219,352,458,565/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 CAVITGAC----ERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 TVSDCAVITGAC-----BRDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Accession: 45.40g-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C;Accession: JG4861
R;Gupta, S.K.; Alves, K.; O'Neil Palladino, L.; Mark, G.E.; Hollis, G.F.
Biochem. Biochem. Biochem. 224, 318-326, 1996
A;Title: Molecular cloning of the human fertilin beta subunit.
A;Reference number: JC4861; MUID:96295488; PMID:8702389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 1574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 734;
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                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   33;
                                                                                                                                                                                                                   A;Experimental source: strain Sprague-Dawley; brain C;Genetics:
A;Gene: MEGF6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.7%; Score 75; DB 2
28.8%; Pred. No. 6.1;
tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                  Query Match
12.8%; Score 75.5; D
Best Local Similarity 28.6%; Pred. No. 10;
Matches 24; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 ETGİCLCİPGEVGSRCQD---TCS 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 KHHTCPCLPNLLCSRFPDGRYRCS 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           453 LPEYCNGSSASCP 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.77
Best Local Similarity 28.88
Matches 21, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: JC4861
A;Molecule type: mRNA
A;Residues: 1-734 <GUP>
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A; Status: preliminary
A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cysteine-rich protein CRP1 - earthworm (Enchytraeus buchholzi)
C;Species: Enchytraeus buchholzi
C;Species: Enchytraeus buchholzi
C;Date: 14-Nov-1994 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession. 455035; 845034
R;Willuhn, J.; Schmitt-Wrede, H.P.; Greven, H.; Wunderlich, F.
J. Biol. Chem. 269, 24688-24691, 1994
A;Title: CDNA cloning of a cadmium-inducible mRNA encoding a novel cysteine-rich, non-me
A;Reference number: A55035; MUID:95014230; PMID:7929141
                                                                                                                 addesive plaque protein Mgfp2 precursor - Mediterranean mussel
C;Species: Mytilus galloprovincialis (Mediterranean mussel)
C;Species: Mytilus galloprovincialis (Mediterranean mussel)
C;Date: 27-Apr-1955 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56175
R;Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.
J. Biol. Chem. 270, 6688-6701, 1995
A;Title: Mussel adhesive plaque protein gene is a novel member of epidermal growth factch A;Reference number: A56175; MUID:95204464; PMID:7896812
                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-473 <INO>
A;Cross-references: UNIPROT:Q25464; GB:D43794; NID:g602767; PIDN:BAA07852.1; PID:d100843
C;Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule_type: mRNA
A;Residues: 1-251 <WIL>
A;Cross-references: UNIPROT:Q24774; EMBL:X79344; NID:g488802; PIDN:CAA55899.1; PID:g4888
C;Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:1-17/Domain: Bignal sequence #status predicted <SIG>
F:387-419/Domain: EGF homology <EGFI>
F:429-460/Domain: EGF homology <EGF>
F:23,36,43,56,75,382,424,455,468,473/Modified site: 3',4'-dihydroxyphenylalanine (Tyr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 SOCKCEKGECKKG--CKEG-CCAPKCGVAGCSCGSGCKCEKGECKPGCTKRCCGTKCGVE 133
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T13954
MEGRé protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13594
E;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O. Genomics 51, 27-34, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECH-PGSHKVPFFRKRKHHTC---PCL
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Pred. No. 1.6;
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30.9%; Pred. No. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ||||: |:|
166 NKGRC--FPDGKTGYKC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 PNLLCSRFPDGR--YRC 96
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Best Local Similarity
Matches 25; Conserv
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us-10-692-299-2.rpr

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A;Title: Rat pancreatic colipase mRNA: nucleotide sequence of a cDNA clone and nutritions A;Reference number: A34623; MUD:90179738; PMID:2129524
A;Accession A34623
A;Accession A34623
A;Accession A34623
A;Accession BNA
A;Residues: 1-17, V, V, 19-112 <WIC>
A;Ross-references: GB:M3333; NID:g203502; PIDN:AAA40943.1; PID:g203503
C;Superfamily: colipase
C;Superfamily: colipase
C;Reywords: lipid digestion; lipid hydrolysis; pancreas
C;Reywords: lipid digestion; lipid hydrolysis; pancreas
F;1-17.Domain: signal sequence #status predicted <SIG>F;11-17.Product: colipase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: CESP:Y64G10A.f
A;Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A35356; A36475; A48416; A36007; A23666; B355010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K. Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and a A;Reference number: A35356; MUID:90260639; PMID:2160731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P20333; GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
*Molecule type: DNA
A;Residues: 1-1620 <WL>
A;Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CABS4471.1; CESP:Y64G10A.f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Y64GlOA.f - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27283
R;Ainscough, R.
submitted to the EMBL Data Library, September 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 RVSIMLLLVTVSDCAVITG------ACERDVQCGAGTCCAISLWLRGLRMCTPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 VSDCAVITGACERDVQCGAG-----TCCAISLWLRGLRMCTPLGREGEECHPGSHKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 12.6%; Score 74; DB 2; Length 112; Local Similarity 25.8%; Pred. No. 1.6; nes 24; Conservative 10; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 GREGEECHPGSHKVPFFRKRKHHTCPCLPNLLC 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 AMENSECSPKTLYGIYYR-----CPCERGLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1149 -----RHSCQCSNGASCDR 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 FFRKRKHHTCPCLPNLLCSR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: clone Y64G10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: Z20336
A;Accession: T27283
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-461 <SMI>
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A35356
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A;Residues: 1-2318 <LAR>
A;Cross-references: UNIPROT:Q61982; EMBL:X74760; NID:g483580; PIDN:CAA52776.1; PID:g4835
C;Superferainly: notch protectin; anixyrin repeat homology; EGF homology
F;163-195/Domain: EGF homology <EGF1>
F;474-505/Domain: EGF homology <EGF2>
F;854-885/Domain: EGF homology <EGF2>
F;854-885/Domain: EGF homology <EGF2>
F;1872-1904/Domain: ankyrin repeat homology <AN1>
F;1872-1904/Domain: ankyrin repeat homology <AN3>
F;1906-1938/Domain: ankyrin repeat homology <AN3>
F;1906-1938/Domain: ankyrin repeat homology <AN3>
F;1906-1938/Domain: ankyrin repeat homology <AN3>
F;19172-2004/Domain: ankyrin repeat homology <AN3>
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Naltenate names: procolipase
C;Species: Rattus norvegicus (Norway rat)
N;Altenate names: procolipase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I51909; A34623
R;Payns, R.M.; Sims, H.F.; Jennens, M.L.; Lowe, M.E.
Am. J. Physiol. 266, G914-G921, 1994
A;Title: Rat pancreatic lipase and two related proteins: enzymatic properties and mRNA e A;Title: Rat pancreatic lipase and two related proteins: enzymatic properties and mRNA e A;Retenne number: I51909; MUID:94262798; PMID:9203536
A;Accession: I51909
A;Accession: I51909
A;Accession: I51909
A;Accession: I512 cPAX'
A;Residues: 1-112 cPAX'
A;Residues: 1-112 cPAX'
A;Residues: UNIPROT:P17084; GB:M58370; NID:g203504; PIDN:AAA20505.1; PID:g203505
B;A;Cross-references: UNIPROT:P17084; GB:M58370; NID:g203504; PIDN:AAA20505.1; PID:g203505
Biochem. Biophys. Res. Commun. 167, 130-136, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            notch homolog - sea urchin (Lytechinus variegatus)

(Species: Lytechinus variegatus (variegated urchin)

(Species: Lytechinus variegatus (variegated urchin)

(Spacession: T31070

R;Sherwood, D.R.; McClay, D.R.

R;Sherwood, D.R.; McClay, D.R.

A;Title: Identification and localization of a sea urchin Notch homologue: insights into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: TSBS
A;Residues: 1-231 cSBS
A;Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.1
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 VDNVCKLEEPCQNGGTCRLTTSLWDYEC-FCTP-ANTGENCTDDNHCV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 CAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC-
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 75;
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28.1%;
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Best Local Similarity 28.1
Matches 25, Conservative
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30; Gaps

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29;

8; Mismatches

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Conservative
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               28;
               Matches
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R; Köhno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990

A; Title: A second tumor necrosis factor receptor gene product can shed a naturally occur A; Reference number: A36475; MUID:91045991; PMID:2172983

A; Reference number: A36475

A; Ratus: preliminary

A; Residues: 1-195, "R., 197-461 < KOH>
A; Residues: 1-195, "R., 197-461 < KOH>
A; Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758

A; Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758

A; Cross-references: GB:M55994; GB:M38549; NID:g339757; Dahm, H.W.; Gentz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990

A; Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A; Reference number: A48416; MUID:91370690; PMID:1966549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA; protein
A; Residues: 23-461 cDEMs
A; Residues: 23-461 cDEMs
A; Cross - references: G8: 863368; NID: g235649; PIDN: AAB19824.1; PID: g235649
A; Note: sequence extracted from NCBI backbone (NCBIN: 63368, NCBIP: 63371)
B; Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Broc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A; Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
A; Reference number: A36007; MUID: 90349572; PMID: 2166946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: B35010
A;Status: preliminary
A;Molecule type: protein
A;Molecule type: protein
A;Kedidues: 27-31 < EMG>
B;Kuhnert, P.; Kemper, O.; Wallach, D.
R;Kuhnert, P.; Kemper, O.; Wallach, D.
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of A;Reference number: I38094; MUID:95121934; PMID:7821811
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C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homold
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
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A; Residues: 23-40; 65-69; 136-141; 300-306 < LOE>
A; Residues: 23-40; 65-69; 136-141; 300-306 < LOE>
B; Engelmann, H; Novick, D; Wallach, D.
B; Biol. Chem. 265, 1531-1536, 1990
A; Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence A; Reference number: A35010; MUID: 90110215; PMID: 2153136
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F;164-201/Domain: NGF receptor repeat homology <NG4>
F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <INT>
F;280-461/Domain: intracellular #status predicted <INT>
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A; Status: preliminary
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A;Status: preliminary
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DB 1; Length 461

Score 73; DB 1 Pred. No. 6.6;

12.4%; 29.5%;

Query Match Best Local Similarity

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R;Nissinen, M.; Vuolteenaho, R.; Boot-Handford, R.; Kallunki, P.; Tryggvason, K. Biochem. J. 276, 369-379, 1991
Biochem. J. 276, 369-379, 1991
A;Title: Primary structure of the human laminin A chain. Limited expression in human tiss A;Reference number: S14663; MUID:91264789; PMID:2049067
A;Accession: S14663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-227, FB', 230-251, MLP', 255-418, 'E', 420-518, 'L', 520-1022,'V', 1024-1074,'V', 1
A; Cross-references: EMBL:X58531; NID:g34225; PIDN:CAA41418.1; PID:g34226
R; Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, 1
Lab. Invest. 60, 772-782, 1989
A; Title: Human laminin: cloning and sequence analysis of CDNAs encoding A, B1 and B2 chan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 chan A;Reference number: A34961; MUID:89280632; PMID:2733383
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LyGene: GDB:LAWA1; LAWA

LyGene: GDB:LAWA1; LAWA

LyGene: GDB:LAWA1; LAWA

LyGene: GDB:L20135; OMIM:150320

LyMap position: 18p1.32-18p1.32-18p1.32

LyMap position: alph1.32-18p1.32-18p1.32

LyMap position: alph1.31-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.32-18p1.
                                                                                                                        98 SRCSSDQVETQACTREQNRICTCRPGWYCALSK-QEGCRLCAPLRKCRPGFGVARPGTET 156
29
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: 51458; 514663; A34961
Matrix 11, 151-160, 1991
A;Title: Molecular cloning of the cDNA encoding human laminin A chain.
A;Reference number: 514458; MUID:91333420; PMID:1714537
----GREGEE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #status atypical <LE6>
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A;Residues: 'W',2397-2745,'L',2747-3053,'L',3055-3072,'PSP' <OLS>
A;Note: the authors translated the codon AGA for residue 2692 as Pro
17 SDCA---VITGACERD----VQCGAGTCCAISLWLRGLRMCTPL
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7742-788/Domain: laminin-type EGF-like homology «LES-
791-846/Domain: laminin-type EGF-like homology «LES-
849-899/Domain: laminin-type EGF-like homology «LES-
902-948/Domain: laminin-type EGF-like homology «LES-
591-995/Domain: laminin-type EGF-like homology «LE10-
998-1041/Domain: laminin-type EGF-like homology «LE112-
                                                                                                                                                                                                                                                                                                                                Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: not compared with conceptual translation
                                                                                                                                                                                                                                                60 -----CHPGSHKVPFFRKRKHHTCPCLPNLLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laminin alpha-1 chain precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: mRNA
A,Residues: 1-3075 <HAA>
A,Cross-references: UNIPROT:P25391
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F;1403-1449/Domain: laminin-type EGF-like homology <LEI8>
F;1452-150/Domain: laminin-type EGF-like homology <LEI8>
F;1509-1553/Domain: laminin-type EGF-like homology <LEI9>
F;1509-1553/Domain: laminin-type EGF-like homology <LEI0>
F;1516-2105/Domain: laminin-type EGF-like homology <LEI0>
F;2142-2300/Domain: aminin G repeat homology <LGI>F;212-2405/Domain: laminin G repeat homology <LGI>F;213-246/Domain: laminin G repeat homology <LGI>F;213-256/Region: cell attachment (R-G-D) motif F;231-2536/Region: cell attachment (R-G-D) motif F;231-2536/Region: cell aminin G repeat homology <LGI-5F;291-2536/Region: laminin G repeat homology <LGI-256/Region: laminin G repeat
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Search completed: September 20, 2005, 12:59:43 Job time : 40 Becs

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